

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2003, 12:00:30 ; Search time 1477 Seconds
(without alignments)
276.978 Million cell updates/sec

Title: US-09-745-763-36_COPY_231_240
Perfect score: 10
Sequence: 1 TACITVEDAE 10

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2688711 seqs, 20454813386 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5764739

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.epool_p/US09745763/runat_23122003_120023_20083/app.query.fasta.1.199
-DB=GenEmbl -OPMT=fastap -SUFFIX=olip2n.rge -MIMMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNTS-bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTMT=ptco
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-Fgapext=7 -Ygapop=60 -Ygapext=60 -DELOP=6 -DELEXT=7

Database : GenEmbl :
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2: gb_Htg :
3: gb_In :
4: gb_Om :
5: gb_Ov :
6: gb_Pat :
7: gb_Ph :
8: gb_Pl :
9: gb_Pr :
10: gb_Ro :
11: gb_Sts :
12: gb_Sy :
13: gb_Un :
14: gb_Vi :
15: em_Ba :
16: em_Fun :
17: em_Hum :
18: em_In :
19: em_Mu :
20: em_Om :
21: em_Or :
22: em_Ov :
23: em_Pat :
24: em_Ph :
25: em_Pl :
26: em_Ro :
27: em_Sts :
28: em_Un :

29: em_Vi :
30: em_Htg_Hum :
31: em_Htg_In :
32: em_Htg_Other :
33: em_Htg_Mus :
34: em_Htg_Pin :
35: em_Htg_Rod :
36: em_Htg_Mam :
37: em_Htg_Vrt :
38: em_Sy :
39: em_Htg_Hum :
40: em_Htg_Mus :
41: em_Htg_Other :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	100.0	1472	9 AF107834	AF107834 Homo sapi
2	100.0	100.0	1596	10 AF107835	AF107835 Mus muscu
3	100.0	100.0	1716	10 AF009513	AF009513 Mus muscu
4	100.0	100.0	1778	6 BD105816	BD105816 Secretary
5	100.0	100.0	1794	9 AF119386	AF119386 Homo sapi
6	100.0	100.0	1796	10 BC037067	BC037067 Mus muscu
7	100.0	100.0	1851	6 BD106411	BD106411 Secretd
8	100.0	100.0	1860	6 AX006440	AX006440 Sequence
9	100.0	100.0	1860	6 BD127520	BD127520 Primer fo
10	100.0	100.0	1860	9 AK075132	AK075132 Homo sapi
11	100.0	100.0	1928	9 BC020689	BC020689 Homo sapi
12	100.0	100.0	144703	9 AP003112	AP003112 Homo sapi
13	100.0	100.0	157927	9 AP006278	AP006278 Homo sapi
14	100.0	100.0	203469	2 AC123654	AC123654 Mus muscu
15	100.0	100.0	214287	2 AC129951	AC129951 Mus muscu
16	70.0	70.0	819	11 BV035880	BV035880 S12P6043
17	70.0	70.0	2000	6 AK655910	AK655910 Sequence
18	70.0	70.0	4560	1 AF060183	AF060183 Mycobacte
19	70.0	70.0	25861	1 AF125999	AF125999 Mycobacte
20	70.0	70.0	27516	1 AY130970	AY130970 Mycobacte
21	70.0	70.0	71286	1 AF143772	AF143772 Mycobacte
22	70.0	70.0	93098	5 AL591389	AL591389 Zebrafish
23	70.0	70.0	99427	2 AP003821	AP003821 Oryza sat
24	70.0	70.0	112182	2 AC141177	AC141177 Rattus no
25	70.0	70.0	131033	5 AL591370	AL591370 Zebrafish
26	70.0	70.0	141707	8 AP005182	AP005182 Oryza sat
27	70.0	70.0	154152	5 AL953886	AL953886 Zebrafish
28	70.0	70.0	157797	8 AP005184	AP005184 Oryza sat
29	70.0	70.0	161370	9 AC093800	AC093800 Homo sapi
30	70.0	70.0	163291	2 AC102390	AC102390 Mus muscu
31	70.0	70.0	173395	2 AP006061	AP006061 Oryza sat
32	70.0	70.0	181773	10 AC087336	AC087336 Mus muscu
33	70.0	70.0	190807	2 AC116586	AC116586 Mus muscu
34	70.0	70.0	199986	10 AC090563	AC090563 Mus muscu
35	70.0	70.0	209143	1 AC134810	AC134810 Rattus no
36	70.0	70.0	212404	10 AC090127	AC090127 Mus muscu
37	70.0	70.0	213347	10 AL831741	AL831741 Mouse DNA
38	70.0	70.0	225054	2 AC101693	AC101693 Mus muscu
39	70.0	70.0	226464	2 AC099442	AC099442 Rattus no
40	70.0	70.0	264110	2 AC122626	AC122626 Rattus no
41	70.0	70.0	270297	2 AC126661	AC126661 Rattus no
42	60.0	60.0	22	6 BD131707	BD131707 Eucaryoti
43	60.0	60.0	239	9 HSA509104	AB0509104 Homo sapi
44	60.0	60.0	240	9 AB067805	AB067805 Homo sapi
45	60.0	60.0	256	10 QRT5	AF090395 Mus muscu

RESULT 1

ALIGNMENTS

AF107834 1472 bp mRNA linear PRI 12-JUL-1999
 LOCUS Homo sapiens clone LCH1 aminopeptidase mRNA, complete cds.
 AF107834
 ACCESSION
 VERSION AF107834.1 GI:5442029
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 (bases 1 to 1472)
 AUTHORS Liu, C.H., Lin, B.Y., and Chang, L.Y.
 TITLE Cloning of the human aminopeptidase gene
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1472)
 AUTHORS Liu, C.H., Lin, B.Y., and Chang, L.Y.
 TITLE Direct Submission
 JOURNAL Submitted (19-NOV-1998) Institute of Biomedical Sciences, Academia Sinica, RM 433, 128, Yen-Chiun-Yuan Road SEC 2, Taipei 11529, Taiwan

FEATURES
 source
 1.1472
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 /mol_type="mRNA"
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 VHLPEPRIPMERGESAVMLEPRHKMILIGSSIGTPPGITAEVLVVSFDELQR
 RASEARGLIVYNOPTGYRTQVGAVEAKVVASLIQSVASFISPTGIQ
 IOEDQGVKIPITACITVEDAMSRMSRGNKIIVHLEMGAKTPTDPSFNTVAITGS
 GSKYPEQVYVSGHLDMDVGGALDDGGAFISWELSLIKDGLRPKRLRLVLTAE
 AEQGGVGAFOYVQLHKVNISYSLVMSDAGTLPGLQPTGSEKARALNEEWSLQ
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CDS
 BASE COUNT 411 a 325 c 381 g 355 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0103 Length: 1472
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AF107834 (1-1472)
 Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
 Db 744 ACAGCCTGTATTACGTCGAGAGACGACGAA 773

RESULT 2
 AF107835 1596 bp mRNA linear ROD 12-JUL-1999
 LOCUS Mus musculus clone LCH-M1 aminopeptidase mRNA, complete cds.
 AF107835
 ACCESSION
 VERSION AF107835.1 GI:5442031
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 1596)
 AUTHORS Liu, C.H., Lin, B.Y., and Chang, L.Y.
 TITLE Cloning of the mouse aminopeptidase gene

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1596)
 AUTHORS Liu, C.H., Lin, B.Y., and Chang, L.Y.
 TITLE Direct Submission
 JOURNAL Submitted (19-NOV-1998) Institute of Biomedical Sciences, Academia Sinica, RM 433, 128, Yen-Chiun-Yuan Road SEC 2, Taipei 11529, Taiwan

FEATURES
 source
 1.1596
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 /clone="LCH-M1"
 /tissue_type="liver"
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 ASEARGLIVYNOPTGYRTQVGAVEAKVVASLIQSVASFISPTGIQ
 KYODGVKIPITACITVEDAMSRMSRGNKIIVHLEMGAKTPTDPSFNTVAITGS
 MYPEEVYVSGHLDMDVGGALDDGGAFISWELSLIKDGLRPKRLRLVLTAE
 ECGGIGASQVYELHKANISKYSLVMSDAGTLPGLQPTGSDKARALNEEWSLQ
 LNTKVPSESGEGTIDINFWIQAGVPGASLRDDLKYKFFHSHSGDTMTVMDPKQNVV
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CDS
 BASE COUNT 415 a 357 c 421 g 403 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.011 Length: 1596
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AF107835 (1-1596)
 Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
 Db 868 ACAGCCTGTATTACGTCGAGAGATGACGAA 897

RESULT 3
 AF009513 1716 bp mRNA linear ROD 01-JUN-1998
 LOCUS Mus musculus hematopoietic lineage switch 2 (HLS2) mRNA, complete
 DEFINITION
 cde.
 ACCESSION AF009513
 VERSION AF009513.1 GI:3169728
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 1716)
 AUTHORS Williams, J.H., Chan, C.-Y., and Klinken, S.P.
 TITLE Hematopoietic lineage switch 2 (HLS2), a novel mRNA species induced
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1716)
 AUTHORS Williams, J.H., Chan, C.-Y., and Klinken, S.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-1997) Biochemistry Department (Laboratory of
 Cancer Medicine), University of Western Australia, Royal Perth
 Hospital, Wellington Street, Perth, WA 6001, Australia

FEATURES
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 1.1716
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 /mol_type="mRNA"
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CDS 97. .1398
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BASE COUNT 476 a 370 c 414 g 456 t

ORIGIN

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Prod. No.: 0.0117 Length: 1716
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AF009513 (1-1716)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
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781 ACAGCCTGATTACGTTAGAAAGATGCAGAA 810

Db

RESULT 4
BD105816
LOCUS BD105816
DEFINITION Secretory protein.
ACCESSION BD105816
VERSION BD105816.1 GI:23200634
KEYWORDS UP 2002502234-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1778)
AUTHORS Jacobs,K., McCoy,J.M., Racie,L.A., Lavallie,E.R., Merberg,D. and Spaulding,V.
TITLE Secretory protein
JOURNAL Patent: JP 2002502234-A 7 22-JAN-2002;
GENETICS INSTITUTE INC
COMMENT PN JP 2002502234-A/7
PD 22-JAN-2002
PF 16-APR-1997 JP 1997537384
PR 18-APR-1996 US 08/634325,13-JAN-1997 US 08/783520 PI
KENNETH JACOBS, JOHN M MCCOY, LISA A RACIE, EDWARD R LAVALLIE, PI
DAVID MERBERG.
PI VIKKI SPAULDING
PC C12N15/12,C07K14/47,A61K38/17
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.

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source 1. .1778 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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ORIGIN

Alignment Scores:
Prod. No.: 0.0121 Length: 1778
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x BD105816 (1-1778)

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707 ACAGCCTGATTATTCGTTGGAAGATGCAGAA 736

Db

RESULT 5
AF119386
LOCUS AF119386
DEFINITION Homo sapiens blood plasma glutamate carboxypeptidase precursor (PGCP) mRNA, complete cds.
ACCESSION AF119386
VERSION AF119386.1 GI:4877697
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1794)
Gingras,R., Richard,C., El-Alfy,M., Morales,C.R., Potier,M. and Pehznetsky,A.V.
Purification, cDNA cloning, and expression of a new human blood N-acetyl-aspartyl-alpha-glutamate plasma glutamate carboxypeptidase homologous to carboxypeptidase/prostate-specific membrane antigen
J. Biol. Chem. 274 (17), 11742-11750 (1999)
99223495
MEDLINE
PUBMED
10206990
2 (bases 1 to 1794)
Gingras,R., Richard,C., El-Alfy,M., Morales,C.R., Potier,M. and Pehznetsky,A.V.
Direct Submision
Submitted (12-JAN-1999) Medical Genetics, Sainte-Justine Hospital, Montreal University, 3175 Cole Sainte-Catherine, Montreal, QU H3T 1C5, Canada

TITLE
JOURNAL
AUTHORS
REFERENCE
MEDLINE
PUBMED
10206990
2 (bases 1 to 1794)
Gingras,R., Richard,C., El-Alfy,M., Morales,C.R., Potier,M. and Pehznetsky,A.V.
Direct Submision
Submitted (12-JAN-1999) Medical Genetics, Sainte-Justine Hospital, Montreal University, 3175 Cole Sainte-Catherine, Montreal, QU H3T 1C5, Canada

FEATURES
source 1. .1794 Location/Qualifiers
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25. .1650
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/db_xref="GI:4877698"
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IOGYODGVPKIPITACTIVEDAMEMSRMASRGKIIIVHLEMGAKTVPDTSF
ISKYPROVVLVSGHLDSDMDVGGGAMDGGAFLSWEALSLIKDGLRPKRLRLV
ABEQSGVGAFOYIQLHKVNIINVSILVMSDAGTFLPTGLOFTGSEKARAIMEV
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ORIGIN
Alignment Scores:
Pred. No.:      0.0122      Length:      1794
Score:          10.00       Matches:      10
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%     Indels:      0
DB:             9           Gaps:        0

US-09-745-763-36_COPY_231_240 (1-10) x AF119386 (1-1794)
Oy      1  ThrAlaCysIleThrValGluAspAlaGlu 10
Db      715 ACAGCCTGATTACCGTGGAAGATGCAGAA 744

RESULT 6
BC037067      1796 bp  mRNA  linear  ROD 16-APR-2003
LOCUS      Mus musculus plasma glutamate carboxypeptidase, mRNA (cDNA clone
DEFINITION
ACCESSION      EC037067
VERSION      EC037067.1  GI:22477497
KEYWORDS      MGC.
SOURCE      Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
              1 (bases 1 to 1796)
REFERENCE
AUTHORS      Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
              Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
              Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
              Hopkins,R.F., Jordan,H., Moore,T., Max,S.T., Wang,J., Heien,F.,
              Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
              Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
              Schaefer,T.E., Brownstein,M.J., Uedlin,T.B., Toshikiyuki,S.,
              Carninci,P., Prange,C., Raha,S.S., Locuelli,N.A., Peters,G.J.,
              Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
              McEwen,R.K.D., Malek,J.A., Gunaratne,P.H., Richards,S.,
              Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
              Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
              Fahey,J., Hellton,E., Kettman,M., Madan,A., Rodighiero,S.,
              Sanchez,A., Whitling,M., Madan,A., Young,A.C., Shevchenko,Y.,
              Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
              Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,U., Myers,R.M.,
              Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
              Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
              Generation and initial analysis of more than 15,000 full-length
              human and mouse cDNA sequences
              Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL      MEDLINE
PUBMED      2388257
              12477932
REFERENCE      2 (bases 1 to 1796)

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AUTHORS      Strausberg,R.
TITLE      Direct Submission
JOURNAL      Submitted (23-AUG-2002) National Institutes of Health, Mammalian
              Gene Collection (MGC), Cancer Genomics Office, National Cancer
              Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
              USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
              Email: gcgaps-remail.nih.gov
              Tissue Procurement: Jeffrey E. Green, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
              Sequencing Center (NISC),
              Galtherburg, Maryland;
              Web site: http://www.nisc.nih.gov/
              Contact: nisc_mgc@nri.nih.gov
              Ahter,N., Ayala,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
              Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
              Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
              Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
              Maduro,Q.L., Masello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
              McDowell,J., Pearson,R., Stantipop,S., Thomas,P.J., Touchman,J.W.,
              Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
              Young,A., Zhang,L.-H. and Green,E.D.
              Clone distribution: MGC clone distribution information can be found
              through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
              Series: IRAP Plate: 81 Row: 9 Column: 18
              This clone was selected for full length sequencing because it
              passed the following selection criteria: matched mRNA gi: 9055233.
              Location/Qualifiers
              1..1796
              /organism="Mus musculus"
              /mol_type="mRNA"
              /strain="FVB/N"
              /db_xref="taxon:10090"
              /clone="MGC:46857 IMAGE:498936"
              /tissue_type="Colon, normal, 5 month old male mouse."
              /clone_1db="NCI CGAP_C024"
              /lab_host="DH10B"
              /note="Vector: pCMV-SPORT6"
              1..1796
              /gene="Pgcp-pending"
              /note="synonyms: HL52, 1190003P12R1k"
              /db_xref="locustid:54381"
              /db_xref="MGI:1889205"
              63..1475
              /codon_start=1
              /product="plasma glutamate carboxypeptidase"
              /protein_id="AA37067.1"
              /db_xref="GI:22477498"
              /db_xref="locustid:54381"
              /translators="MRSLEFLTVHLLALGSGAIVKNGVSGRTFREIKEELIANVEDV
              AKAIIPHERGESAVMLEPRIRKHAALIGLSISCTPGCIAEVLVAVSPELOR
              LEORVIRPHERGESAVMLEPRIRKHAALIGLSISCTPGCIAEVLVAVSPELOR
              ASERAKIIVNPPYGVKTYRQVGAVEAKVAVASLIOSVAFSISPTGIG
              KYDGPRIPTACTITVEDAMSRMASRKNKVIYIHEMAKTYPPDPSFRTVAIGS
              MYPEEVLVSGHDSWDVQAGALDDGGAFISWEALSLVADDLRFRKRLRLVLTBE
              EQGIGASVYEELHAKNIKISYSLVMSADGFLPTGLQFTGSKARAKIMEVNLLOP
              LNTKTFSSNGEGRDINFWIOAGVPGASLRDLIDLYKYFFFHSHSDITVMDPKQMNVA
              AVAAVAVVAVDMDLPPRS"
BASE COUNT      526 a 372 c 418 g 480 t
ORIGIN
Alignment Scores:
Pred. No.:      0.0122      Length:      1796
Score:          10.00       Matches:      10
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%     Indels:      0
DB:             10          Gaps:        0

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US-09-745-763-36_COPY_231_240 (1-10) x BC037067 (1-1796)

Qy 1 ThralaCysileThryValgluAspAlaGlu 10
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 Db 747 ACAGCCTGTATTACGTTGGAAGATGCAGAA 776

RESULT 7
 BD106411 1851 bp DNA linear PAT 18-SEP-2002

LOCUS Secreted proteins and polynucleotides encoding them.

ACCESSION BD106411
 VERSION BD106411.1 GI:23201229
 KEYWORDS JP 2002503955-A/2.

SOURCE Chlamydia sp.
 ORGANISM Chlamydia sp.

REFERENCE 1 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 1 (bases 1 to 1851)

AUTHORS Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
 Treacy,M., Spaulding,V. and Agostino,M.J.

TITLE Secreted proteins and polynucleotides encoding them
 JOURNAL Patent: JP 2002503955-A 2 05-FEB-2002;
 GENETICS INSTITUTE INC

COMMENT PN JP 2002503955-A/2
 PD 05-FEB-2002
 PF 20-MAR-1998 JP 1998545874
 PR 21-MAR-1997 US 08/822167,19-MAR-1998 US 09/044466 PI
 KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE,PI
 DAVID MERBERG,
 PI MAURICE TREACY,VIRKI SPAULDING,MICHAEL J AGOSTINO PC
 C12N15/12,C07K14/47,A61K38/17
 CC Strandedness: Double;
 CC Topology: Linear;
 FH Key Location/Qualifiers.

FEATURES
 source 1..1851
 /organism="Chlamydia sp."
 /mol_type="genomic DNA"
 /db_xref="taxon:35827"

BASE COUNT 531 a 413 c 438 g 469 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0125 Length: 1851
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x BD106411 (1-1851)

Qy 1 ThralaCysileThryValgluAspAlaGlu 10
 |||||
 Db 789 ACAGCCTGTATTACGTTGGAAGATGCAGAA 818

RESULT 8
 AX006440 1860 bp DNA linear PAT 06-SEP-2000

LOCUS Sequence 5 from Patent WO0004157.
 ACCESSION AX006440
 VERSION AX006440.1 GI:9994575

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Neefs,J.M., Peeters,D.C. and Pangalos,M.
 Cloning and characterization of novel mammalian peptidases
 Patent: WO 0004157-A 5 27-JAN-2000;
 JANSSEN PHARMACEUTICA NV (BE); NEEFS JEAN MARC EDMOND FERNAND (BE);
 PEETERS DANIELLE CELINE GEORGE (BE); PANGALOS MENIAS (GB)

TITLE Cloning and characterization of novel mammalian peptidases
 JOURNAL Location/Qualifiers

FEATURES
 source 1..1860
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 515 a 423 c 451 g 471 t
 ORIGIN

source 1..1860
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 518 a 420 c 451 g 471 t
 ORIGIN

Alignment Scores:

Pred. No.: 0.0126 Length: 1860
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AX006440 (1-1860)

Qy 1 ThralaCysileThryValgluAspAlaGlu 10
 |||||
 Db 815 ACAGCCTGTATTACGTTGGAAGATGCAGAA 844

RESULT 9
 BD127520 1860 bp DNA linear PAT 18-SEP-2002

LOCUS Primer for synthesizing full-length cDNA and use thereof.
 DEFINITION BD127520
 ACCESSION BD127520
 VERSION BD127520.1 GI:23222465
 KEYWORDS JP 2002017375-A/2951.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1860)
 Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
 Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
 Koga,H.

TITLE Primer for synthesizing full-length cDNA and use thereof
 JOURNAL Patent: JP 2002017375-A 2951 22-JAN-2002;
 HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)
 PN JP 2002017375-A/2951
 PD 22-JAN-2002
 PF 07-JUL-2000 JP 2000253172.

PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
 PI ISHII,
 PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
 SHINICHI KOJIMA,
 PI TETSUJI OTSUKI,HISASHI KOGA
 PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
 10', C12P21/02,C12P1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key

FEATURES
 source 1..1860
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 515 a 423 c 451 g 471 t
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Alignment Scores:
 Pred. No.: 0.0126 Length: 1860
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x BD127520 (1-1860)

Oy 1 ThrAlaCyellThrValGluAspAlaGlu 10
 DB 819 ACAGCCTGTATTACGCTGGAAGATCAGAA 848
 RESULT 10
 LOCUS AK075132
 DEFINITION Homo sapiens cDNA FLJ90651.f1a, clone PLACE1004482, moderately similar to Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA.
 ACCESSION AK075132
 VERSION AK075132.1 GI:22761022
 KEYWORDS oligo capping, f1s (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Isegai,T., Oca,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahara,K., Masuno,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hatton,A., Okumura,K., Iwayanagi,T. and Nimomiya,K.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1860)
 AUTHORS Isegai,T. and Otsuki,T.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-2002) Takao Isegai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
 FEATURES
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 /db_xref="taxon:9606"
 /clone="PLACE1004482"
 /tissue_type="placenta"
 /clone_lib="PLACE1"
 /note="Cloning vector: PME18SFL3"
 129..1547
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="BAC11423.1"
 /db_xref="GI:22761023"
 /translation="MKFLIFAFPGVHLLSLCSGKAIKNGISKRTFEEIEEIEASCG DVAKAIINLAIVYGAKNSYERLALLVDVGPRLSGSKNLEKAIQIMYONLOQDGLK VHAEPRIPIHMERGESAVMLBPRIKIAILIGSSIGTPREGITAEVLVTSFDELO RRAEARGKIVVYNOPYINYSRVOYRTGAVAAAGALASLIRSVASISYSPHG IOEYQDGVKPIPTACTIVEDAEEMSMASHGKITIVQLKNGATTPDTSFNTVAET GSKYPRQVAVLVSGHDSMDVQGAMDGGGAFISWEALSLIKDLGLRPKRTLLVLT AEQGGVGAFOYQYLHKVNI SNYSLVMSDAGFLPGLOFTGSEKARAI VEEWMSLL OPNITOVLSHGEGTDINFMIQAGVPGASLLDLYKKYFFHHSHGDTMTVMDEKQNV AAAVVAIVSVVADMEMLPRS"
 CDS
 BASE COUNT 515 a 423 c 451 g 471 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.0126 Length: 1860
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AK075132 (1-1860)
 Oy 1 ThrAlaCyellThrValGluAspAlaGlu 10
 DB 819 ACAGCCTGTATTACGCTGGAAGATCAGAA 848
 RESULT 11
 LOCUS BC020689
 DEFINITION Homo sapiens, plasma glutamate carboxypeptidase, clone MGC:22418
 IMAGE:4251802, mRNA, complete cds.
 ACCESSION BC020689
 VERSION BC020689.1 GI:18088383
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 CNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNU)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.sbgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNU at: <http://image.llnl.gov>
 Series: IRAL Plate: 35 Row: F Column: 13
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7706386.
 FEATURES
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 /mol_type="mRNA"
 /db_xref="LocusID:10404"
 /db_xref="taxon:9606"
 /clone="MGC:22418 IMAGE:4251802"
 /tissue_type="Skin, melanotic melanoma, high MDR."
 /clone_lib="NIH_MGC_62"
 /lab_host="DH10B"
 /note="vector: pDNR-LIB"
 167..1585
 /codon_start=1
 /product="plasma glutamate carboxypeptidase"
 /protein_id="AAH20689.1"
 /db_xref="GI:18088384"
 /translation="MKFLIFAFPGVHLLSLCSGKAIKNGISKRTFEEIEEIEASCG DVAKAIINLAIVYGAKNSYERLALLVDVGPRLSGSKNLEKAIQIMYONLOQDGLK VHAEPRIPIHMERGESAVMLBPRIKIAILIGSSIGTPREGITAEVLVTSFDELO RRAEARGKIVVYNOPYINYSRVOYRTGAVAAAGALASLIRSVASISYSPHG IOEYQDGVKPIPTACTIVEDAEEMSMASHGKITIVQLKNGATTPDTSFNTVAET GSKYPRQVAVLVSGHDSMDVQGAMDGGGAFISWEALSLIKDLGLRPKRTLLVLT AEQGGVGAFOYQYLHKVNI SNYSLVMSDAGFLPGLOFTGSEKARAI VEEWMSLL OPNITOVLSHGEGTDINFMIQAGVPGASLLDLYKKYFFHHSHGDTMTVMDEKQNV AAAVVAIVSVVADMEMLPRS"
 CDS
 BASE COUNT 554 a 435 c 466 g 473 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.013 Length: 1928

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Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x BC020689 (1-1928)

Qy 1 ThrAlaCysGleThrValGluAspAlaGlu 10
Db 857 ACAGCCTGATTAAGTGGAAGATGCAGAA 886

RESULT 12
AP003112 144703 bp DNA linear PRI 23-JAN-2001
LOCUS Homo sapiens genomic DNA, chromosome 8q23, clone:KB1288E10.
ACCESSION AP003112
VERSION AP003112.1 GI:12362038
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 144703)
AUTHORS Shimizu, N. and Asakawa, S.
TITLE Homo sapiens chromosome clone KB1288E10 on 8q23
REFERENCE 2 (bases 1 to 144703)
AUTHORS Shimizu, N. and Asakawa, S.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2001) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail: nshimizu@db.med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
FEATURES
source
1. 144703
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8q23"
/clone="KB1288E10"
/cell_line="FLEB14-14"
/clone_lib="Keio BAC library"
complement(703..787)
repeat_region
/evidence=not_experimental
/rpt_family="L2"
1336..1358
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/rpt_family="AT_rich"
1795..1923
/evidence=not_experimental
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1938..1972
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1977..2010
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/rpt_family="GA-rich"
2107..2127
/evidence=not_experimental
/rpt_family="AT_rich"
2330..2461
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2610..2781
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/rpt_family="(TGA)n"
complement(12904..3189)
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4349..4387
/evidence=not_experimental

repeat_region
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4536..4722
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4733..4762
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/rpt_family="(TAA)n"
complement(5484..5587)
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/rpt_family="L2"
5676..5773
/evidence=not_experimental
/rpt_family="L2"
7168..7197
/evidence=not_experimental
/rpt_family="AT_rich"
7564..7941
/evidence=not_experimental
/rpt_family="MLT1J"
9319..9461
/evidence=not_experimental
/rpt_family="MER5A"
complement(9568..9659)
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complement(9753..9816)
/evidence=not_experimental
/rpt_family="MIR"
10160..10394
/evidence=not_experimental
/rpt_family="MIR"
11183..11207
/evidence=not_experimental
/rpt_family="(T)n"
complement(11712..12064)
/evidence=not_experimental
/rpt_family="MER46B"
12191..12226
/evidence=not_experimental
/rpt_family="AT_rich"
complement(12307..12368)
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13149..13170
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/rpt_family="AT_rich"
complement(13957..16674)
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complement(17261..17480)
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complement(17609..17916)
/evidence=not_experimental
/rpt_family="A1uSg"
complement(18026..18258)
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/rpt_family="MIR"
19212..19287
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19824..20169
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20170..20228
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20229..20575
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complement(20761..20809)
/evidence=not_experimental
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repeat_region complement(20810..21215)
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repeat_region complement(21216..21319)
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/rpt_family="MIR"
repeat_region 21384..21508
/evidence=not_experimental
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repeat_region complement(22420..22961)
/evidence=not_experimental
/rpt_family="LIME1"
repeat_region 23730..23999
/evidence=not_experimental
/rpt_family="L2"
repeat_region complement(24677..25078)
/evidence=not_experimental
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repeat_region 25365..25641
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repeat_region complement(26245..26363)
/evidence=not_experimental
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repeat_region complement(26859..26986)
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repeat_region complement(27671..27898)
/evidence=not_experimental
/rpt_family="MER20"
repeat_region 28238..28394
/evidence=not_experimental
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repeat_region complement(29127..29655)
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repeat_region complement(31494..31550)
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repeat_region complement(32594..32807)
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repeat_region complement(33191..33329)
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repeat_region 33494..33991
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repeat_region 37083..37430
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/rpt_family="MER46B"
repeat_region 37858..37954
/evidence=not_experimental

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Alignment Scores:
Pred. No.: 0.564 Length: 144703
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-745-763-36_COPY_231_240 (1-10) x AP003112 (1-144703)
Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
Db 19498 ACAGCTGTATTACGTGGAAGATGCAGAA 19527

RESULT 13
LOCUS AP006278 157927 bp DNA linear PRI 25-MAR-2003
DEFINITION Homo sapiens genomic DNA, chromosome 8q22.1, clone: KB1573B4,
complete sequence.
ACCESSION AP006278
VERSION AP006278.1 GI:29170583
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Shimizu,N. and Asakawa,S.
TITLE Homo sapiens DNA chromosome 8 SEQUENCE
JOURNAL Published Only in Database (2003)
REFERENCE 2 (bases 1 to 157927)
AUTHORS Shimizu,N. and Asakawa,S.
TITL Direct Submission
JOURNAL Submitted (24-MAR-2003) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail:nshimizu@med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)

FEATURES
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/clone_lib="Keio BAC library"
103..202
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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US-09-745-763-36_COPY_231_240 (1-10) X AP006278 (1-157927)

1 ThrAlaCysIleThrValGluAspAlaGlu 10

Db 14425 ACAGCCTGTATTACCGTGAAGATGCAGAA 144454

RESULT 14

AC123654

DEFINITION μ_{mus} musculus clone RP23-161D16, WORKING DRAFT SEQUENCE, 6 unordered

ACCESSION AQ123654

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; CONTACT: [redacted]

ORGANISM

PREFERENCE

AUHOKS
 Birren, B., Nussbaum, C. and Lander, B.
 TITTE
 Mus musculus clone PP23-161N16

REFERENCE 2 (pages 1 to 203469)
JOURNAL UNPUBLISHED

Anderson, S., Barna, N., Bastien, V.,
Britten, B., Dutton, D., Hubbard, C.,

Faro, S., Ferreira, P.,

Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,

Lamazares, R., Landers, T., Lehoczký, J., Levine, R., Lindblad-To

Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,

Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill D., Oliver J, Peterson K, Rhuband P, Dierckx N

POLLARA, V., Raymond, C., Retta, R., Riley, R., Rise, R., Roman, J., Rosetti, M., Roy, A., Santos, P., Schauer, S., Bocoy, P.

Schuppback, R., Seaman, S., Severy, P., Spencer, B., Stange-Tinoman
Stojanovic N Strauss N Subramanian A Talamas J Tesfay

Vassiliev, H., Voevodsky, A., Wilson, B., Wu, X., Wyman, D., Ye, J.

TITLE
Young, G., Zarnowski, D., Ziemer, A. and Zou, M.
Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepe

Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro,

Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

[illegible]

Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Bhukha, P., Piore, N.

Roman, I., Schauer, S., Schurback, B., Seaman, S., Severy, P., Smi-
kachupka, A., Ramasamy, U., Raymond, C., Ketta, R., Rise, C., Kogo

Spencer, B., Stojanovic, N., Stubbs, M.,
Tajamas, Y., Tesfaye, S., Theodore, J., Totham, K., Travers, M.,

Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody

JOURNAL Submitted (11-MAR-2003) whitehead Institute/MIT Center for Genomics

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 11, 2003 this sequence version replaced gi:28630056
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)

----- Genome Center
 Center: Whitehead Institute/MIT Center for Genome

Center: Walter and Annita Jones Center for Genome Research
Center code: WJBR
Web site: <http://www.cga.wisc.edu>

Project Information
Contact: sequence_submissions@genome.wi.mit.edu
web site: <http://www-seq.wi.mit.edu>

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%

Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AC123654 (1-203469)

QY 1 ThrAlaCyseIleThrValGIuAspAlaGlu 10
 Db 37215 ACAGCCTGTATTCACAGTAAAGATGCAGAA 37244

RESULT 15 AC129951 214287 bp DNA linear HTG 06-MAR-2003
 AC129951/c Mus musculus clone RP23-127B14, WORKING DRAFT SEQUENCE, 5 unordered pieces.

ACCESSION AC129951 GI:28667103
 VERSION AC129951.3
 KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 214287)
 AUTHORS Birren,B., Nusbaum,C. and Lander,E.
 TITLE Mus musculus, clone RP23-127B14
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 214287)

AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barta,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karakas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Menus,L., Milnova,T., Menga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,F., O'Neill,D., Oliver,J., Peterson,K., Phunhthang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,D., Testfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.

REFERENCE 3 (bases 1 to 214287)
 TITLE Direct Submission
 JOURNAL Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelell,A., Allen,N., Anderson,S., Arachchi,H.M., Barta,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., Dearrellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Fero,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karakas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Menus,L., Milnova,T., Menga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,F., O'Neill,D., Oliver,J., Peterson,K., Phunhthang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Testfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.

TITLE
 JOURNAL

COMMENT

On Mar 6, 2003 this sequence version replaced gi:28604146. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/XM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L26330
 Center clone name: 127_B_14

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 213323 bases at least Q40
 Consensus quality: 213594 bases at least Q30
 Consensus quality: 213779 bases at least Q20
 Insert size: 21000; agarose-fp
 Insert size: 213887; sum-of-ctigs
 Quality coverage: 8.3 in Q20 bases; agarose-fp
 Quality coverage: 8.2 in Q20 bases; sum-of-ctigs

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 96711: contig of 96711 bp in length
 * 96712 96811: gap of 100 bp
 * 96812 113998: contig of 1787 bp in length
 * 113999 114098: gap of 100 bp
 * 114099 138884: contig of 24786 bp in length
 * 138885 138984: gap of 100 bp
 * 138985 210099: contig of 7115 bp in length
 * 210100 210199: gap of 100 bp
 * 210200 214287: contig of 4088 bp in length.

FEATURES

source

1. 214287
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
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 misc_feature 114099..138884
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 misc_feature 138985..210099
 /note="assembly_fragment"
 misc_feature 210200..214287
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 clone_end=T7
 vector_side="right"

BASE COUNT 67592 a 41331 c 41087 g 63872 t 405 others
 ORIGIN

Alignment Scores:

Pred. No.: 0.794 Length: 214287
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AC129951 (1-214287)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
|||
Db 94648 ACAGCTGTATCATCACAGTGAAGATGCAGAA 94619

Search completed: December 23, 2003, 13:06:21
Job time : 1517 secs

and is derived by analysis of the total score distribution

105.447 Million cell updates/sec

Title: US-09-745-763-36_COPY_231_240

Sequence: 1 TACITVEDAE 10

Scoring table: OLIGO

Ygapop 60.0 , Ygapext 60.0

Delop	6.0	, Delext	7.0
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Searched: 2552756 seqs, 1349719017 residues

Word size:

Total number of hits satisfying chosen parameters: 5087518

Minimum DB seq length: 0

1

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-USER=US09745763 @CGN_1_1_490 @runat_23122003_120023_20072 -NCFE

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEX
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Pred. No. is the number of results predicted by chance to

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2	10	100.0	1134	21	AAZ98101	Human secreted pro
3	10	100.0	1134	22	AAD11714	Human secreted pro
4	10	100.0	1134	24	ABK69810	Human secreted pro
5	10	100.0	1134	25	ACC50818	Human secreted pro
6	10	100.0	1134	25	ABZ71454	Secreted protein-e
7	10	100.0	1767	21	AAA40493	Human fetal kidney
8	10	100.0	1778	18	AAV02292	Human secreted pro
9	10	100.0	1784	23	AA573592	DNA encoding novel
10	10	100.0	1851	19	AAV82779	Clone hu45.2 isolat
11	10	100.0	1851	24	ABO92016	Human polynucleoti
12	10	100.0	1860	22	AAK94491	Human full-length
13	10	100.0	1863	21	AAZ98034	Human secreted pro
14	10	100.0	1863	22	AAD11647	Human secreted pro
15	10	100.0	1863	24	ABK69743	Human secreted pro
16	10	100.0	1863	25	ACC50817	Human secreted pro
17	10	100.0	1864	25	ABZ71453	Secreted protein-e
18	10	100.0	1884	21	AAZ58313	Human peptidase NA
19	10	100.0	1895	22	AAH99703	Human protein enco
20	10	100.0	1923	21	AAZ98139	Human signal pepti
21	10	100.0	2077	25	ACC50603	Human secreted pro
22	10	100.0	2077	25	ABZ71131	Secreted protein-e
23	6	60.0	22	20	AAH86568	PCR primer used to
24	6	60.0	37	22	AAF72789	Human atonal homol
25	6	60.0	297	20	ABK76373	Bacillus lichenifco
26	6	60.0	300	20	AAV90208	EST clone DF591.
27	6	60.0	382	21	AAC28786	Human secreted pro
28	6	60.0	391	22	AA537015	Novel human diagno
29	6	60.0	434	22	AA159253	Human polynucleoti
30	6	60.0	456	22	ABA43344	Human breast cell
31	6	60.0	456	22	ABA53784	Human foetal liver
32	6	60.0	456	22	ABA23533	Probe #199 for ge
33	6	60.0	456	22	AAK02047	Human brain express
34	6	60.0	456	22	AAK27504	Human bone marrow
35	6	60.0	456	22	AAI12079	Probe #2012 for ge
36	6	60.0	456	22	AAI33417	Probe #2103 used t
37	6	60.0	456	22	AAI02003	Probe #1994 used t
38	6	60.0	456	23	AB527069	Human liver singlet
39	6	60.0	524	24	ABL81845	Human ovarian canc
40	6	60.0	536	21	AAA26906	Essential Staphylo
41	6	60.0	536	22	AA508057	Staphylococcus aur
42	6	60.0	536	22	AAAF91588	Staphylococcus aur
43	6	60.0	609	22	AAF72620	Human atonal homol
44	6	60.0	612	24	ABK24523	EIF-2alpha kinase
45	6	60.0	641	22	AAH52191	Human olfactory re

ALIGNMENTS

RESULT 1

ID AAA44369 standard; cDNA; 895 BP.

AC AAA44369;

DT 21-AUG-2000 (first entry)

DE Human secreted expressed tag SEQ ID NO:944

KW Human; mouse; chicken; rat; secreted expressed sequence tag; SEST,

KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;

KW antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;

KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;

KM vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
 KM insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
 KM lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
 KM central nervous system disorder; Alzheimer's disease; stroke;
 KM Parkinson's disease; Huntington's disease; coagulation disorder;
 KM hemophilia; thrombosis; inflammatory disorder; Crohn's disease;
 KM tumour; infection; depression; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200021991-A1.
 PD 20-APR-2000.
 XX
 PF 15-OCT-1999; 99WO-US24206.
 XX
 PR 15-OCT-1998; 98US-0104436.
 XX
 PA (GEMV) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
 PI Metberg D, Treacy M, Bowman MR;
 XX
 DR WPI: 2000-317938/27.
 XX
 PT Isolated polynucleotides, and encoded proteins, comprising secreted
 PT expressed sequence tags (ESTs), useful for treating various disorders
 PT such as autoimmune, infectious, and central nervous system disorders -
 XX
 PS Claim 1; Page 446; 803bp; English.
 XX
 CC AAA43426 to AAA45925 represent specifically claimed secreted expressed
 CC sequence tags (ESTs), isolated from human, mouse, chicken and rat
 CC tissue sources. The ESTs can have a range of activities depending on
 CC the tissues they were isolated from. The activities include:
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
 CC cyostatic; antibacterial; antifungal; antiviral; antidiabetic;
 CC antiaesthetic; vulnary; antileuk; osteoprotective; neuroprotective;
 CC nociceptive; antiparkinsonian; antipsoriatic; cerebroprotective;
 CC anticonvulsant; and antidepressant. The ESTs can be used for gene
 CC therapy and in vaccines. The ESTs are useful as probes for the
 CC identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the ESTs. Proteins encoded by the ESTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (hemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 895 BP; 274 A; 195 C; 224 G; 201 T; 1 other;

Alignment Scores:
 Pred. No.: 0.01 Length: 895
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 10
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AAA44369 (1-895)
 Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
 Db 734 ACACCCCTGATTTACGCGTGAAGATGACGAA 763
 RESULT 2
 AA298101

ID AA298101 standard; cDNA; 1134 BP.
 XX
 AC AA298101;
 XX
 DT 09-MAY-2000 (first entry)
 XX
 DE Human secreted protein encoding nucleotide sequence SEQ ID NO:95.
 XX
 KM Human; secreted protein; diagnostic; cyostatic; immunosuppressive;
 KM antiinflammatory; nociceptive; neuroprotective; antiallergic; cancer;
 KM tumour; neurodegenerative disorder; developmental abnormality; allergy;
 KM foetal deficiency; blood disorder; immune system disorder; arthritis;
 KM autoimmune disease; hepatic disease; renal disease; inflammation;
 KM Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis;
 KM infection; AIDS; spinal cord injury; transplant rejection; diabetes;
 KM asthma; sepsis; acne; psoriasis; cardiovascular disorder;
 KM reproductive disorder; gastrointestinal disorder; respiratory disorder;
 KM metabolic disorder; food additive; preservative; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200004140-A1.
 PD 27-JAN-2000.
 XX
 PF 14-JUL-1999; 99WO-US15849.
 XX
 PR 15-JUL-1998; 98US-0092921.
 PR 15-JUL-1998; 98US-0092922.
 PR 15-JUL-1998; 98US-0092956.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Komatsoulis G, Duan RD, Rosen CA, Moore PA, Shi Y;
 PI Lafleur DW, Edder R, Olsen HS, Brewer LA, Florence KA, Young PB;
 PI Mucenski M, Endress GA, Soppet DR;
 DR WPI: 2000-161128/14.
 DR P-PSDB; AA67148.
 XX
 PT New isolated human genes, useful for diagnosis and treatment of, e.g.
 PT cancers, neurological or blood disorders -
 XX
 PS Claim 1; Page 365; 494bp; English.
 XX
 CC The polynucleotide sequences given in AA298017 to AA298108 encode the
 CC human secreted proteins given in AA187064 to AA187223. Human secreted
 CC protein can have activities based on the tissues and cells the genes are
 CC expressed in. Examples of activities include: cyostatic;
 CC immunosuppressive; antiinflammatory; nociceptive; neuroprotective; and
 CC antiallergic. The polynucleotides and their corresponding secreted
 CC polypeptides are useful for preventing, treating or ameliorating medical
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions
 CC can be diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the new
 CC polynucleotides. Human secreted protein s and their polynucleotides can
 CC be used for developing products for the diagnosis or treatment of cancer.
 CC tumours, neurodegenerative disorders, developmental abnormalities and
 CC foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, hepatic and renal diseases, inflammation,
 CC allergies, Alzheimer's disease, behavioural disorders, schizophrenia,
 CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,
 CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,
 CC cardiovascular disorders, reproductive disorders, gastrointestinal
 CC disorders, respiratory disorders and metabolic disorders. The
 CC proteins or polynucleotides can also be used as food additives or
 CC preservatives. The proteins are also useful for identifying their
 CC binding partners. AA298008 to AA298016 and AA187063 are sequence used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 1134 BP; 333 A; 247 C; 250 G; 304 T; 0 other;

Alignment Scores:

Pred. No.: 0.0123 Length: 1134
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AA298101 (1-1134)
 QY 1 ThrAlaCyeIleThrValGluAspAlaGlu 10
 Db 61 ACAGCCTGTATTACGGTGAAGATGCAGAA 90

RESULT 3
 AAD11714
 ID AAD11714 standard; cDNA; 1134 BP.
 AC AAD11714;
 XX 24-SEP-2001 (first entry)
 DT
 XX Human secreted protein-encoding gene 18 cDNA clone HMA234, SEQ ID NO:95.
 DE
 XX Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
 KW porphyrin; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;
 KW angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
 KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
 KW cell culture; chemotaxis; vulnery; binding partner identification;
 KW gene therapy; ss.
 KM
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 687..788
 FT /*tag= a
 FT /product= "Human secreted protein precursor"
 FT
 XX WO200151504-A1.
 PN 19-JUL-2001.
 XX
 PD 12-JAN-2001; 2001WO-US00911.
 XX
 PF 13-JAN-2000; 2000US-0482273.
 XX
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Ruben SM, Komatsoulis GA, Duan DR, Rosen CA, Moore PA, Shi Y,
 PI Lafleur DM, Olsen HS, Brewer LA, Florence KA, Young PE, Soppet DR;
 PI Endress GA, Muscenski M, Ebner R;
 XX
 XX WPI: 2001-425865/45.
 DR P-PSDB; AAE06125.
 DR
 XX Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -
 XX
 XX Claim 1; Page 732; 864pp; English.
 PS
 XX AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted
 CC protein genes, and AAE06041-AAE06132 represent the proteins they encode.
 CC AAE06133-AAE06205 represent human secreted protein fragments.
 CC The secreted proteins and their genes are useful for preventing, treating
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 71 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative

CC disorders, cancer, tumours, foetal and developmental abnormalities,
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, autoimmune
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
 CC The present sequence represents a human secreted protein-encoding cDNA of
 CC the invention.
 XX
 SO Sequence 1134 BP; 333 A; 247 C; 250 G; 304 T; 0 other;

Alignment Scores:
 Pred. No.: 0.0123 Length: 1134
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AAD11714 (1-1134)
 QY 1 ThrAlaCyeIleThrValGluAspAlaGlu 10
 Db 61 ACAGCCTGTATTACGGTGAAGATGCAGAA 90

RESULT 4
 ABE69810
 ID ABE69810 standard; cDNA; 1134 BP.
 AC ABE69810;
 XX
 DT 15-JUL-2002 (first entry)
 DT
 XX Human secreted protein gene 18 #2.
 DE
 XX Human; ss; gene; secreted protein; gene therapy; immunosuppressive;
 KW antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;
 KW vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
 KW virucide; fungicide; ophthalmological; autoimmune disease; neoplasm;
 KW rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
 KW cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
 KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; wound healing; skin aging;
 KW epithelial cell proliferation; food additive.
 KM
 OS Homo sapiens.
 XX
 PN WO200226931-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 24-SEP-2001; 2001WO-US29871.
 XX
 PR 25-SEP-2000; 2000US-234925P.
 XX
 PR 12-JAN-2001; 2001WO-US00911.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Ruben SM, Komatsoulis G, Duan DR, Rosen CA, Moore PA, Shi Y,
 PI Lafleur DM, Olsen H, Brewer LA, Florence KA, Young PE, Soppet DR,
 PI Endress GA, Mucenski M, Ebner R;
 XX

DR WPI; 2002-362489/39.
DR P-PSDB; ABG33947.
XX
PT Novel 71 isolated secreted polypeptides and polynucleotides encoding
PT the polypeptides, useful for treating Huntington's disease, sepsis,
PT meningitis, thrombocytopenia, haemolytic anaemia, rheumatoid arthritis,
PT asthma
PS Claim 1; Page 1213-1214, 1478pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (or its
CC fragment, homologue complement or allelic variant) encoding a human
CC secreted protein (and its fragment, domain, epitope, variant, secreted
CC form and species variant). Also included are a recombinant vector
CC comprising the nucleic acid, a recombinant host cell comprising the
CC vector, an antibody against the secreted protein, a recombinant host cell
CC that expresses the secreted protein and a method of identifying a binding
CC partner of the secreted protein. The nucleic acid and protein are used to
CC prevent, diagnose, treat or ameliorate a medical condition in e.g.
CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep
CC for example autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. Many other diseases and
CC disorders are listed in the specification. The polypeptides can also be
CC used to aid wound healing an epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. The present
CC sequence encodes a novel human secreted protein of the invention.
XX
SQ Sequence 1134 BP; 333 A; 247 C; 250 G; 304 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 0.0123 Length: 1134
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-745-763-36_COPY_231_240 (1-10) x ABK69810 (1-1134)
CY 1 ThrAaCysIleThrValGluAspAlaGlu 10
Db 61 ACAGCCGTGATTACGGTGAAGATGCAGAA 90
RESULT 5
ACCS0818
ID ACCS0818 standard; cDNA; 1134 BP.
XX
AC ACCS0818;
XX
DT 12-JUN-2003 (first entry)
DE Human secreted protein coding sequence, SEQ ID 485.
XX
KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytoskeletal;
KW vulnery; antiinflammatory; nootropic; neuroprotective;
KW antiparkinsonian; gene therapy; human; cardiovascular disorder;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO200295010-A2.
XX
PD 28-NOV-2002.
XX
PF 19-MAR-2002; 2002WO-US09785.
XX

PR 21-MAR-2001; 2001US-277340P.
PR 19-JUL-2001; 2001US-306171P.
PR 13-NOV-2001; 2001US-331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-129429/12.
XX
XX
PT Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating
PT cardiovascular disorders such as arrhythmia
PS Claim 21; SEQ ID 485; 1881pp; English.
XX
XX The present invention relates to novel human secreted proteins
CC (ABR47633-ABR48145) and their coding sequences (ACCS0344-ACCS0856). The
CC proteins and their coding sequences are useful for the preparation of a
CC diagnostic or pharmaceutical composition for diagnosing or treating a
CC cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,
CC coronary arteriosclerosis and myocardial ischaemia), neural disorders,
CC immune system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism.
CC Note: The sequence data for this patent was published in electronic
CC format and is available from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1134 BP; 333 A; 247 C; 250 G; 304 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 0.0123 Length: 1134
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0
US-09-745-763-36_COPY_231_240 (1-10) x ACCS0818 (1-1134)
CY 1 ThrAaCysIleThrValGluAspAlaGlu 10
Db 61 ACAGCCGTGATTACGGTGAAGATGCAGAA 90
RESULT 6
ABZ71454
ID ABZ71454 standard; cDNA; 1134 BP.
XX
AC ABZ71454;
XX
DT 04-APR-2003 (first entry)
DE Secreted protein-encoding gene 142 cDNA clone HRACU35, SEQ ID NO:275.
XX
XX Human; secreted protein; digestive disorder; gastrointestinal disorder;
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
KW immune disorder; inflammation; infection; wound healing; drug screening;
KW chromosome identification; chromosome mapping; cytoskeletal;
KW antiinflammatory; immunosuppressive; vulnery; gene therapy; gene; ss.

XX Homo sapiens.
 OS
 XX
 PN MO200276488-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 19-MAR-2002; 2002WO-US08276.
 XX
 PR 21-MAR-2001; 2001US-277340P.
 PR 19-JUL-2001; 2001US-306171P.
 PR 13-NOV-2001; 2001US-331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-029900/02.
 DR P-PSDB; ABR00275.
 XX
 PT New human secreted proteins and nucleic acids, useful for detecting,
 PT preventing, diagnosing, prognosticating, creating and/or ameliorating
 PT e.g. gastrointestinal diseases and disorders, or cancers -
 XX
 PS Claim 21; Page 918-919; 1216pp; English.
 XX
 CC ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted
 CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.
 CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
 CC invention also encompasses antibodies specific for the secreted proteins,
 CC the use of the secreted proteins in drug screening, and recombinant
 CC vectors and host cells comprising a nucleic acid of the invention. The
 CC secreted proteins, nucleic acids encoding them, antibodies or antibody
 CC fragments specific for the secreted proteins, and modulators of protein
 CC activity are useful for diagnosing, treating, ameliorating or preventing
 CC digestive disorders. Such conditions include disorders of the mouth,
 CC oesophagus, stomach, small intestine, large intestine, liver, biliary
 CC tract and pancreas, and include cancers of these organs and tissues. The
 CC secreted proteins and their nucleic acids may also be used in the
 CC treatment of immune disorders, inflammation, infection,
 CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
 CC of the invention may be used for chromosome identification, chromosome
 CC mapping, in gene therapy, for identifying individuals from minute
 CC biological samples, as hybridisation probes, and as molecular weight
 CC markers. The present sequence represents a human secreted protein-
 CC encoding cDNA clone of the invention.
 CC
 SQ Sequence 1134 BP; 333 A; 247 C; 250 G; 304 T; 0 other;
 Alignment Scores:
 Pred. No.: 0.0123 Length: 1134
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0
 US-09-745-763-36_COPY_231_240 (1-10) x ABZ71454 (1-1134)
 QY 1 ThralaCyse11eThrVal1GluAspAlaGlu 10
 Db 61 ACAGCCTGTTTACGGTGGAAAGATGCAGAA 90
 RESULT 7
 ID AAA40493 standard; cDNA; 1767 BP.
 XX AAA40493;
 AC
 XX AAA40493;
 XX 16-NOV-2000 (first entry)
 XX Human fetal kidney cDNA fragment AM282_11.
 DE
 XX

KM Secreted protein; cytosolic; immunostimulatory; antimicrobial;
 KM antiviral; immunosuppressive; antiinflammatory; vulnery; cytokine;
 KM cell proliferation; differentiation; regulatory; treatment; tumor;
 KM autoimmune disease; inflammatory disorder; wound; microbial infection;
 KM viral disease; graft versus host reaction suppression; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200037630-A1.
 XX
 PD 29-JUN-2000.
 XX
 PF 22-DEC-1999; 99WO-US31005.
 XX
 PR 23-DEC-1998; 98US-0220876.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C,
 PI Merberg D, Treacy M, Bowman MR;
 XX
 DR WPI; 2000-442661/38.
 DR P-PSDB; AAB10229.
 XX
 PT Secreted human proteins AS296-11 and AS34-11, useful for treating
 PT tumors, autoimmune diseases, inflammatory disorders, wounds, microbial
 PT infections and viral diseases -
 XX
 PS Disclosure; Page 198; 293pp; English.
 XX
 CC This invention describes novel secreted human proteins (I) which have
 CC cytostatic, immunostimulatory, antimicrobial, antiviral,
 CC immunosuppressive, antiinflammatory and vulnery activity and which act
 CC as cytokine, cell proliferation or differentiation regulators. (I)
 CC is useful for treating tumors, autoimmune diseases, inflammatory
 CC disorders, wounds, microbial infections and viral diseases. (I) is also
 CC useful for suppressing graft versus host reaction. AAA40490-AA0580
 CC represent cDNA fragments that encode the secreted proteins
 CC AAB10226-B10288 described in the method of the invention.
 CC
 SQ Sequence 1767 BP; 512 A; 384 C; 418 G; 453 T; 0 other;
 Alignment Scores:
 Pred. No.: 0.0179 Length: 1767
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-745-763-36_COPY_231_240 (1-10) x AAA40493 (1-1767)
 QY 1 ThralaCyse11eThrVal1GluAspAlaGlu 10
 Db 696 ACAGCCTGTTTACGGTGGAAAGATGCAGAA 725
 RESULT 8
 ID AAV02296 standard; DNA; 1778 BP.
 XX AAV02296;
 AC
 XX AAV02296;
 XX 21-MAY-1998 (first entry)
 XX Human secreted protein AM282 full-length cDNA clone.
 XX Secreted protein; AM282; cytokine; human; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 17..1435
 FT CDS /*tag= a

XX Human, chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PP 30-MAR-2001; 2001WO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HYSR-) HYSRQ INC.
 XX
 XX Drmanac RT, Liu C, Tang YT;
 DR WPI, 2001-639362/73.
 DR P-PSDB; ABG09405.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 XX Claim 1; SEQ ID No 9396; 103bp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations in
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 1784 BP; 508 A; 389 C; 426 G; 461 T; 0 other;
 SQ
 Alignment Scores:
 Score: 0.018 length: 1784
 Aired. No.: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 23 Gaps: 0
 US-09-745-763-36_COPY_231_240 (1-10) x AAS73592 (1-1784)
 OY 1 ThrAlaCysIleThrValGluAspAlaGlu 10
 Db 691 ACAACCTGTTTACGGTGAAGATGCAGAA 720
 RESULT 10
 ID AAV82779 standard; cDNA; 1851 BP.
 XX AAV82779;
 XX

DT 25-FEB-1999 (first entry)
 XX
 XX Clone hu45_2 isolated from human adult placenta cDNA library.
 DE
 XX Secreted protein; nutritional activity; immune stimulating; vaccine;
 XX suppressing activity; haematopoiesis regulating activity;
 XX tissue growth activity; activin; inhibin activity; chemotaxis;
 XX chemokinetic activity; haemostasis; thrombolytic activity; receptor;
 XX ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
 XX tumour inhibition; gene therapy; ds.
 OS
 XX Homo sapiens.
 PN MO9842739-A2.
 XX
 XX 01-OCT-1998.
 PD
 XX 20-MAR-1998; 98WO-US05653.
 PF
 XX 19-MAR-1998; 98US-0044466.
 PR 21-MAR-1997; 97US-0822167.
 XX
 XX (GENY) GENETICS INST INC.
 PA Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Spaulding V, Treacy M;
 XX
 XX WPI; 1998-609890/51.
 DR P-PSDB; AAW85456.
 XX
 XX New polynucleotide encoding secreted human proteins - derived from
 PT human foetal brain, adult brain, foetal kidney, placenta or adult
 PT pineal gland cDNA libraries.
 XX
 XX Claim 14; Page 69-70; 113pp; English.
 PS
 XX The present sequence encodes a secreted protein. The polynucleotide and
 CC secreted protein are predicted to have biological activities which would
 CC make them suitable for treating, preventing or ameliorating medical
 CC conditions in humans and animals, although no supporting data is given.
 CC Suggested activities include nutritional activity, immune stimulating
 CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemokinetic/chemokinetic activity, haemostatic and thrombolytic activity,
 CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
 CC invasion suppressor activity, and tumour inhibition activity (no data is
 CC given in the specification to support these activities). The
 CC polynucleotide is also stated to be useful for gene therapy.
 XX
 XX Sequence 1851 BP; 531 A; 413 C; 438 G; 469 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 0.0186 Length: 1851
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 19 Gaps: 0
 US-09-745-763-36_COPY_231_240 (1-10) x AAV82779 (1-1851)
 QY 1 ThrAlaCysIleTrrValGluAspAlaGlu 10
 Db 789 ACAGCCTGTATTACGGTGAAGATGCAGAA 818
 RESULT 11
 ABQ92016 ID ABQ92016 standard; cDNA; 1851 BP.
 XX
 AC ABQ92016;
 XX
 DT 04-OCT-2002 (first entry)
 XX

DE Human polynucleotide SEQ ID NO 13.
 XX
 XX Human; cytostatic; antirheumatic; antiarthritic; vulnery; analgesic;
 XX antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
 XX neuroprotective; nootropic; osteopathic; haemostatic; vasotropic;
 XX antitumor; fungicide; antidiabetic; antiallergic;
 XX immunostimulant; antiparasitic; secreted protein; transmembrane protein;
 XX cytokine; cell proliferation; cell differentiation; autoimmune disease;
 XX stem cell; growth factor; nervous system disease; neuropathy;
 XX Alzheimer's disease; Parkinson's disease; Huntington's disease;
 XX osteoporosis; severe combined immunodeficiency; SCID; infection;
 XX multiple sclerosis; rheumatoid arthritis; gene therapy; gene; ss.
 OS
 XX Homo sapiens.
 PN US2002065394-A1.
 XX
 XX 30-MAY-2002.
 PD
 XX 22-DEC-2000; 2000US-0745763.
 PF
 XX 18-MAR-1998; 98US-0040963.
 PR
 XX (JACO/) JACOBS K.
 PA (MCCO/) MCCOY J M.
 PA (LAVA/) LAVALLIE E R.
 PA (COLL/) COLLINS-RACIE L A.
 PA (EVAN/) EVANS C.
 PA (MERB/) MERBERG D.
 PA (TREAC/) TREACY M.
 PA (SPAUD/) SPAULDING V.
 XX
 XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Spaulding V;
 XX
 XX WPI; 2002-582343/62.
 DR P-PSDB; ABP61800.
 XX
 XX Novel secreted or transmembrane protein and polynucleotide encoding the
 PT protein, useful for diagnosis and treatment of neurological disorders,
 PT cancer, autoimmune diseases, bone disorders and lung or liver fibrosis
 PT
 XX
 XX Claim 50; Page 113-114; 284pp; English.
 PS
 XX The invention relates to human secreted or transmembrane protein (I),
 CC their fragments and is encoded by specific complementary deoxyribonucleic
 CC acid (cDNA) inserts (II), where the protein is substantially free from
 CC other mammalian proteins. (I) are useful for preventing, treating or
 CC ameliorating a medical condition, especially immunological treatment or
 CC prevention of tumours. (I) exhibits activity relating to angiogenesis,
 CC cytokine, cell proliferation, cell differentiation, antiinflammatory,
 CC stem cell growth factor activity and activin or inhibin-related
 CC activities. (I) can be used to manipulate stem cells in culture to give
 CC rise to neuroepithelial cells that can be used to augment or replace
 CC cells damaged by illness, autoimmune disease, accidental damage or
 CC genetic disorders. (I) induces the proliferation of neural cells and
 CC regeneration of nerve and brain tissue and is useful for the treatment of
 CC central and peripheral nervous system diseases and neuropathies, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopaenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or
 CC periodontal disease. (I) is also useful for gut protection or
 CC regeneration and treatment of lung or liver fibrosis, reperfusion injury
 CC in various tissues, various immune deficiencies and disorders including
 CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
 CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
 CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,
 CC such as asthma or other respiratory problems. (II) is useful to express

CC recombinant protein, as markers for tissues in which the corresponding
CC protein is preferentially expressed and in gene therapy. The present
CC sequence is that of a polynucleotide of the invention.

XX Sequence 1851 BP; 531 A; 413 C; 438 G; 469 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	Matches:
Score:	0.0186	1851
Percent Similarity:	100.00%	10
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	100.00%	Mismatches: 0
DB:	24	Indels: 0
		Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AB92016 (1-1851)

Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
Db 789 ACAGCCTGTATTACGGTGAAGATGCAGAA 818

RESULT 12

ID AAK94491 standard; cDNA; 1860 BP.

XX AAK94491;

DT 06-NOV-2001 (first entry)

XX Human full-length cDNA, SEQ ID NO: 3328.

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

PN EP1130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-0114089.

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI: 2001-524255/58.

XX P-PSDB: AAM93559.

PT 830 Primers useful for synthesizing full length cDNA clones and their

XX use in genetic manipulation -

PS Claim 8; SEQ ID NO 3328; 1380bp + sequence listing; English.

CC The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been

CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA

CC cDNA are useful for clarifying the function of the protein encoded by

CC the cDNA. The full length clones were obtained by construction of full

CC length enriched cDNA libraries that were synthesized by the oligo-capping

CC method. The primers enable the production of the full length cDNA easily

CC without any special methods. The present sequence is a full length

Pred. No.:	Length:	Matches:
Score:	0.0187	1860
Percent Similarity:	100.00%	10
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	100.00%	Mismatches: 0
DB:	22	Indels: 0
		Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AAK94491 (1-1860)

Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
Db 819 ACAGCCTGTATTACGGTGAAGATGCAGAA 848

RESULT 13

ID AAZ98034 standard; cDNA; 1863 BP.

XX AAZ98034;

DT 09-MAY-2000 (first entry)

XX Human secreted protein encoding nucleotide sequence SEQ ID NO:28.

KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;

KW antiinflammatory; nootropic; neuroprotective; antiallergic; cancer;

KW tumour; neurodegenerative disorder; developmental abnormality; allergy;

KW foetal deficiency; blood disorder; immune system disorder; arthritis;

KW autoimmune disease; hepatic disease; renal disease; inflammation;

KW Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis;

KW infection; AIDS; spinal cord injury; transplant rejection; diabetes;

KW asthma; sepsis; acne; psoriasis; cardiovascular disorder;

KW reproductive disorder; gastrointestinal disorder; respiratory disorder;

KW metabolic disorder; food additive; preservative; ss.

XX Homo sapiens.

PN WO200004140-A1.

PD 27-JAN-2000.

PF 14-JUL-1999; 99WO-US15849.

PR 15-JUL-1998; 98US-0092921.

PR 15-JUL-1998; 98US-0092922.

PR 15-JUL-1998; 98US-0092956.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Komatsoulis G, Duan RD, Rosen CA, Moore PA, Shi Y;

PI Lafleur DM, Ebner R, Olsen HS, Brewer LA, Florence KA, Young PE;

PI Mucenki M, Endress GA, Soppet DR;

DR WPI: 2000-161128/14.

XX P-PSDB: AAY87081.

PT New isolated human genes, useful for diagnosis and treatment of, e.g.

XX cancers, neurological or blood disorders -

PS Claim 1; Page 319; 494bp; English.

CC The polynucleotide sequences given in AAZ98017 to AAZ98108 encode the

CC human secreted proteins given in AAY87064 to AAY87223. Human secreted

CC protein can have activities based on the tissues and cells the genes are

CC expressed in. Examples of activities include: cytostatic; neuroprotective; and

CC immunosuppressive; antiinflammatory; nootropic; neuroprotective; and

CC antiallergic. The polynucleotides and their corresponding secreted

CC polypeptides are useful for preventing, treating or ameliorating medical

CC conditions, e.g. by protein or gene therapy. Also pathological conditions

CC can be diagnosed by determining the amount of the new polypeptides in a

CC sample or by determining the presence of mutations in the new

CC polynucleotides. Human secreted protein s and their polynucleotides can

CC be used for developing products for the diagnosis or treatment of cancer,

CC tumours, neurodegenerative disorders, developmental abnormalities and

Alignment Scores:

CC foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation,
CC allergies, Alzheimer's disease, behavioural disorders, schizophrenia,
CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,
CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,
CC cardiovascular disorders, reproductive disorders, gastrointestinal
CC disorders, respiratory disorders and metabolic disorders. The
CC proteins or polynucleotides can also be used as food additives or
CC preservatives. The proteins are also useful for identifying their
CC binding partners. AAZ98008 to AAZ98016 and AA87063 are sequence used in
CC the exemplification of the present invention.

SQ Sequence 1863 BP; 533 A; 417 C; 443 G; 470 T; 0 other;

Alignment Scores:	
Pred. No.:	0.0187
Score:	10.00
Percent Similarity:	100.00%
Best local Similarity:	100.00%
Query Match:	100.00%
DB:	21
Length:	186
Matches:	10
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-745-763-36_COPY_231_240 (1-10) X AAZ98034 (1-1863

OY 1 ThrAlaCyStIeThrValGIuAspAlaGlu 10
 |||||
Dd 789 ACAGCGTGTATTACGGTGGAAGATGCAGAA 818

RESULT 14
AAD11647
ID AAD11647 standard; cDNA; 1863 BP

DT 24-SEP-2001 (first entry)

DE Human secreted protein-encoding gene 18 cDNA clone HRACJ35, SEQ ID NO:28

KM Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KM foetal abnormality; developmental abnormality; haematopoietic disorder;
KM immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KM Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KM psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KM inflammation; neurological disorder; Alzheimer's disease; food additive;
KM angiodenic disorder; kidney disorder; gastrointestinal disorder; allergy;
KM pregnancy-related disorder; endocrine disorder; infection; wound healing
KM cell culture; chemotaxis; vulnery; binding partner identification;
KM gene therapy; ss.

OS Homo sapiens

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
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100	100	100

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PN WO200151504-A1

PD 19-JUL-2001.

PF 12-JAN-2001; 2001WO-US00911.

PR 13-JAN-2000; 2000US-0482273.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Komatsoulis GA, Duan DR, Rosen CA, Moore PA, Shi Y;

PI Endress GA, Muscenski M, Ebner R;
vxy

DR WPI; 2001-425865/45.
DB P-PEDP; AAF060E9

DR P-PSDB; AAE06058.

PT Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition -

PS Claim 1; Page 686; 864pp; English.

CC AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted
CC protein genes, and AAE06041-AA060132 represent the proteins they encode
CC AAE06133-AA060205 represent human secreted protein fragments.
CC The secreted proteins and their genes are useful for generating transgenic
CC mice expressing and their genes are useful for generating transgenic mice

CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 71 genes,
CC based on the tissues in which they are most highly expressed, and included
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, focal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiotensin disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA)
CC the present sequence represents a human secreted protein-encoding cDNA of
CC the invention.

SQ Sequence 1863 BP; 533 A; 417 C; 443 G; 470 T; 0 other;

Alignment Scores:

Pred. No.:	0.0187	Length:	1
Score:	10.00	Matches:	1
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-745-763-36_COPY_231_240 (1-10) X AAD11647 (1-1863)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
|||
Db 789 ACAGCGTGTATACGGTGGAAGATGCAGAA 818

RESULT 15

ID ABK69743 standard; cDNA; 1863 BP

AC ABK69743;

DT 15-JUL-2002 (first entry

DE Human secreted protein gene 18 #1

KW Human; ss; gene; secreted protein; gene therapy; immunosuppressive;

KW vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial,

KW rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;

KW, angiogenesis; nervous system disorder; Alzheimer's disease; infection;

KM ocular disorder; corneal infection; wound healing; skin aging;
KM epithelial cell proliferation; food additive.

OS Homo sapiens.

PN WO200226931-A2.

XX 04-APR-2002.

PD 24-SEP-2001; 2001WO-US29871.

XX 25-SEP-2000; 2000US-234925P.

PR 12-JAN-2001; 2001WO-US00911.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Komatsoulis G, Duan DR, Rosen CA, Moore PA, Shi Y;

PI Lafleur DW, Olsen H, Brewer LA, Florence KA, Young PE, Soppet DR;

PI Endress GA, Mucenski M, Ebner R;

DR WPI: 2002-362489/39.

DR P-PSDB; ABG33880.

PT Novel 71 isolated secreted polypeptides and polynucleotides encoding

PT the polypeptides, useful for treating Huntington's disease, sepsis,

PT meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,

PT asthma

PS Claim 1; Page 1170; 1478pp; English.

XX The invention relates to an isolated nucleic acid molecule (or its

CC fragment, homologue complement or allelic variant) encoding a human

CC secreted protein (and its fragment, domain, epitope, variant, secreted

CC form and species variant). Also included are a recombinant vector

CC comprising the nucleic acid, a recombinant host cell comprising the

CC vector, an antibody against the secreted protein, a recombinant host cell

CC that expresses the secreted protein and a method of identifying a binding

CC partner of the secreted protein. The nucleic acid and protein are used to

CC prevent, diagnose, treat or ameliorate a medical condition in e.g.

CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep

CC for example autoimmune diseases e.g. rheumatoid arthritis,

CC hyperproliferative disorders e.g. neoplasms of the breast or liver,

CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders

CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.

CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and

CC ocular disorders e.g. corneal infection. Many other diseases and

CC disorders are listed in the specification. The polypeptides can also be

CC used to aid wound healing an epithelial cell proliferation, to prevent

CC skin aging due to sunburn, to maintain organs before transplantation, for

CC supporting cell culture of primary tissues, to regenerate tissues and in

CC chemotaxis. The polypeptides can also be used as a food additive or

CC preservative to increase or decrease storage capabilities. The present

CC sequence encodes a novel human secreted protein of the invention.

XX

SQ Sequence 1863 BP; 533 A; 417 C; 443 G; 470 T; 0 other;

XX

Alignment Scores:

Pred. No.: 0.0187 Length: 1863

Score: 10.00 Matches: 10

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 24 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x ABK69743 (1-1863)

OY 1 ThrAlaCysIleThrValGluAspAlaGlu 10

Db 789 ACAGCCTGTATACGTGAGATGACGAA 818

Search completed: December 23, 2003, 12:39:26
Job time : 259 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2003, 12:00:30 / Search time 2046 Seconds
(without alignments)
118.790 Million cell updates/sec

Title: US-09-745-763-36_COPY_231_240
Sequence: 1 TACTIVEDAE 10

Scoring table:
OLIGO
Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues
Word size: 1
Total number of hits satisfying chosen parameters: 45557478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Command line parameters:
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-cgn2_1/USPTO.spool.p/US09745763/runat_23122003_120024_20097/app_query.faeta_1.199
-DB=EST-QPMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=quality -THR MIN=1 -MODE=LOCAL -OUTFMT=pro
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :
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3: em_estin: *
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5: em_estrov: *
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9: gb_est1: *
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11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
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28: gb_gss1: *

29: gb_gss2: *
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	174	9	AA790960
2	10	100.0	296	9	AA329616
3	10	100.0	313	10	BE833868
4	10	100.0	314	13	EX091504
5	10	100.0	317	10	BE833878
6	10	100.0	320	10	BE833882
7	10	100.0	334	10	BE833866
8	10	100.0	362	9	AA790981
9	10	100.0	442	9	AI021522
10	10	100.0	443	9	AA634903
11	10	100.0	443	9	AA611336
12	10	100.0	463	9	AI050369
13	10	100.0	475	9	AA105255
14	10	100.0	504	9	AA452391
15	10	100.0	524	13	BU696863
16	10	100.0	528	13	BU694506
17	10	100.0	544	10	AM952474
18	10	100.0	576	12	BM256759
19	10	100.0	592	13	BU695545
20	10	100.0	637	13	BO564473
21	10	100.0	650	10	BG432644
22	10	100.0	653	10	BE218907
23	10	100.0	662	14	BY747978
24	10	100.0	676	9	AA796802
25	10	100.0	677	10	BE670671
26	10	100.0	707	10	BF119418
27	10	100.0	708	14	CD366462
28	10	100.0	739	14	CB958693
29	10	100.0	752	14	W28330
30	10	100.0	793	14	CB234306
31	10	100.0	794	14	CD356404
32	10	100.0	804	14	CD352906
33	10	100.0	813	14	CD519131
34	10	100.0	866	13	BU146905
35	10	100.0	902	10	BE751497
36	10	100.0	909	13	BQ878966
37	10	100.0	919	13	EX335995
38	10	100.0	926	13	BO938234
39	10	100.0	998	13	BA460463
40	10	100.0	1012	13	EX416896
41	10	100.0	1024	11	BC012019
42	10	100.0	1038	10	BX355940
43	10	100.0	1050	13	EX439467
44	10	100.0	1739	11	AK032972
45	10	100.0	1805	11	AK075686

ALIGNMENTS

RESULT 1	AA790960	174 bp	mRNA	linear	EST 06-FEB-1998
LOCUS	AA790960				
DEFINITION	AA790960				
ACCESSION	AA790960				
VERSION	AA790960.1				
KEYWORDS	EST				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 174)				

AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gaisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE
 The WashU-HMNI Mouse EST Project

JOURNAL
 Unpublished

COMMENT
 Contact: Marra M/Mouse EST Project
 WashU-HMNI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:658000
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 82.

FEATURES
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 /mol_type="mRNA"
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 /clone="IMAGE:1244312"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stage="4 weeks"
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 /note="Organ: mammary gland; Vector: pT73D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dt) primer [5', TGTTACCAATCTGAGTGGAGCGCCGCGATGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
 46 a 42 c 41 g 44 t 1 others

ORIGIN

Alignment Scores:
 Pred. No.: 0.00216 Length: 174
 Score: 10.00 Matches: 10
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AA790960 (1-174)

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 1 ThrAlaCysGtTThrValGluAspAlaGlu 10
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 118 ACAGCCTGTATCACAGTAGAATGACGAA 147

RESULT 2
 AA329616 296 bp mRNA linear EST 20-APR-1997
 LOCUS BE833868 296 bp mRNA linear EST 20-APR-1997
 DEFINITION BE833868 Embryo, 12 week II Homo sapiens cDNA 5' end, mRNA
 ACCESSION AA329616
 VERSION AA329616.1 GI:1981858
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 296)
 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

Cy
 1 ThrAlaCysGtTThrValGluAspAlaGlu 10
 |||||
 61 ACAGCCTGTATTCAGGTGAGATGACGAA 90

RESULT 3
 BE833868/c 313 bp mRNA linear EST 22-SEP-2000
 LOCUS BE833868 313 bp mRNA linear EST 22-SEP-2000
 DEFINITION BE833868 RC6-OT0076-220500-012-B07 OT0076 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE833868
 VERSION BE833868.1 GI:10266246
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 313)
 Dias Neco, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

TITLE
 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL
 Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE
 96026280

PUBMED
 7566098

COMMENT
 Other ESTs: THC171697
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 source
 1..296
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):131268"
 /db_xref="taxon:9606"
 /dev_stage="Embryo, 12 wks"
 /clone_lib="Embryo, 12 week II"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT
 84 a 62 c 79 g 69 t 2 others

ORIGIN

Alignment Scores:
 Pred. No.: 0.00374 Length: 296
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AA329616 (1-296)

TITLE
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.U.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE
20202663

PUBMED
10737800

COMMENT
Contact: Simpson A.U.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-27049922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml.pl?file=RC6-OT0076-220
500-012-B07&f3=2000-05-22&f4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 313
Location/Qualifiers

FEATURES
source
1..313
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="OT0076"
/note="Organ: ovary; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
, 716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT
70 a 80 c 76 g 87 t

ORIGIN

Alignment Scores:
Pred. No.: 0.00397 Length: 313
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

DB: 10

US-09-745-763-36_COPY_231_240 (1-10) x BE833868 (1-313)

Qy
1 ThralAcysileThrValGluAspAlaGlu 10
|||||
171 ACAGCCTGTATTACGTGAGATGACGAA 142
|||||

Db
171 ACAGCCTGTATTACGTGAGATGACGAA 142
|||||

RESULT 4
BX091504 314 bp mRNA linear EST 23-JAN-2003
BX091504 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone
IMAGE:796263, mRNA sequence.

LOCUS
BX091504

DEFINITION
IMAGE:796263, mRNA sequence.

ACCESSION
BX091504

VERSION
BX091504.1 GI:27826297

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 314)
Ebert, L., Hell, O., Hennig, S., Neubert, P., Patsch, E., Peters, M.,
Radejof, U., Schneider, D. and Korn, B.

REFERENCE
1 (bases 1 to 314)
Ebert, L., Hell, O., Hennig, S., Neubert, P., Patsch, E., Peters, M.,
Radejof, U., Schneider, D. and Korn, B.

AUTHORS
Ebert, L., Hell, O., Hennig, S., Neubert, P., Patsch, E., Peters, M.,
Radejof, U., Schneider, D. and Korn, B.

TITLE
Human Unigeneset - RZPD3

JOURNAL
Unpublished

COMMENT
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD, IMAGE:796263.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No. 972)
http://www.rzpd.de/ClonesCards/cgi-
bin/showlib.pl.cgi?response=11&No=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAAACGCTATGAC.
Location/Qualifiers

FEATURES
source
1..314
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:796263"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_1lb="Soares total fetus Nb2HF8 9w"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dt) primer (5'
TGTTCCAACTGAGTGGAGCGCGCTATTATTTTATTTT 3').
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
88 a 64 c 87 g 73 t

ORIGIN

Alignment Scores:
Pred. No.: 0.00398 Length: 314
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

DB: 13

US-09-745-763-36_COPY_231_240 (1-10) x BX091504 (1-314)

Qy
1 ThralAcysileThrValGluAspAlaGlu 10
|||||
35 ACAGCCTGTATTACGTGAGATGACGAA 64
|||||

Db
35 ACAGCCTGTATTACGTGAGATGACGAA 64
|||||

RESULT 5
BE833878 317 bp mRNA linear EST 22-SEP-2000
RC6-OT0076-220500-012-E04 OT0076 Homo sapiens cDNA, mRNA sequence.

LOCUS
BE833878

DEFINITION
BE833878

ACCESSION
BE833878

VERSION
BE833878.1 GI:10266256

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 317)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.U.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

REFERENCE
1 (bases 1 to 317)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.U.

AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.U.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=RC6-OT0076-220
 500-012-504&ct3=2000-05-22&ct4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 11
 High quality sequence stop: 317.
 Location/Qualifiers
 1..317
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="OT0076"
 /note="Organ: ovary; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 71 a 84 c 76 g 86 t
ORIGIN
 Alignment Scores:
 Pred. No.: 0.00402 Length: 317
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-745-763-36_COPY_231_240 (1-10) x BE833878 (1-317)
Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
 ||||||||||||||||||||||||||||||||
Db 175 ACAGCCTGTATTCGCTGAGATGCAGAA 146
 ||||||||||||||||||||||||||||||||
RESULT 6
BE833882/c 320 bp mRNA linear EST 22-SEP-2000
LOCUS BE833882
DEFINITION RC6-OT0076-220500-012-F03 OT0076 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE833882
VERSION BE833882.1 GI:10266260
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=RC6-OT0076-220
 500-012-F03&ct3=2000-05-22&ct4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 10
 High quality sequence stop: 320.
 Location/Qualifiers
 1..320
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="OT0076"
 /note="Organ: ovary; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 73 a 83 c 75 g 89 t
ORIGIN
 Alignment Scores:
 Pred. No.: 0.00406 Length: 320
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-745-763-36_COPY_231_240 (1-10) x BE833882 (1-320)
Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
 ||||||||||||||||||||||||||||||||
Db 178 ACAGCCTGTATTCGCTGAGATGCAGAA 149
 ||||||||||||||||||||||||||||||||
RESULT 7
BE833866/c 334 bp mRNA linear EST 22-SEP-2000
LOCUS BE833866
DEFINITION RC6-OT0076-220500-012-A10 OT0076 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE833866
VERSION BE833866.1 GI:10266244
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922

Fax: +55-11-2707001
 Email: aseimpo@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=at2-RG6-OT0076-220
 500-012-A10&t3=2000-05-22&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 38
 High quality sequence stop: 334.
 Location/Qualifiers

FEATURES

Source
 1.334
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="adult"
 /clone_lib="OT0076"
 /note="Organ: ovary; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue RNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 77 a 86 c 80 g 91 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.00425 Length: 334
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x BE833866 (1-334)

Cy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
 |||||
 Db 192 ACAGCCTGATTACGTCGAGAGATGCAGAA 163

RESULT 8 AA790981 362 bp mRNA linear EST 06-FEB-1998
 LOCUS AA790981
 DEFINITION IMAGE:1244408 5', mRNA sequence.

ACCESSION AA790981 GI:2851101
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Mus musculus (house mouse)
 EST.

REFERENCE AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 362)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The Washu-HMI Mouse EST Project
 JOURNAL Unpublished
 COMMENT Contact: Marra M/Mouse EST Project
 Washu-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

FEATURES
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:658096
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 321.
 Location/Qualifiers

source

1.362
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="IMAGE:1244408"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DRI0B"
 /lab_host="DRI0B"
 /clone_lib="Soares_mammary_gland_NbMWG"
 /note="Organ: mammary gland; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCACTGCAAGTGGAGCGCCGCAATGTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 97 a 74 c 97 g 93 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 0.00462 Length: 362
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AA790981 (1-362)

Cy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
 |||||
 Db 118 ACAGCCTGATTACAGTAGAAGATGCAGAA 147

RESULT 9 AI021522 442 bp mRNA linear EST 16-JUN-1998
 LOCUS AI021522
 DEFINITION IMAGE:1366450 5', mRNA sequence.

ACCESSION AI021522 GI:3235858
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Mus musculus (house mouse)
 EST.

REFERENCE AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 442)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The Washu-HMI Mouse EST Project
 JOURNAL Unpublished
 COMMENT Contact: Marra M/Mouse EST Project
 Washu-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

FEATURES
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:899670
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 431.
 Location/Qualifiers
 1.442

[illegible]

/clone="IMAGE:842076"

/sex="male"

/dev_stage="72 years"

/lab_host="SOLR cells (kanamycin resistant)"

/clone_1lb="Stratagene lung (#937210)"

*/note="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI
dt_normal_lung. Average insert size: 1.0 kb; Uni-ZAP XR
Vector: -5 adaptor sequence: 5' GAATTCGGCAGACG 3'
adaptor sequence: 5' CTCGACTTCTTTTTTTTTTTTTT 3'"*

BASE COUNT 112 A 95 C 126 G 109 T 1 others

ORIGIN

Alignment Scores:

Pred. No.: 0.00569 Length: 443

Score: 10.00 Matches: 10

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AA634903 (1-443)

CY 1 ThrLacysIethrValGluaSPAlaGlu 10

Dn 107 ACACCCTGTATTACGTGAAGAATGCAGAA 136

RESULT 11

LOCUS AA461136 443 bp mRNA linear EST 09-JUN-1997

DEFINITION ZK64F08.R1 Soares_total_fetus_Nb2HFg_9w Homo sapiens cDNA clone

ACCESSION AA461136 IMAGE:796263 5', mRNA sequence.

VERSION AA461136.1 GI:2186256

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 443)
Hallier L., Allen M., Bowles J., Dubugue T., Geisler G., Joist S.,
Knocaba T., Lucy M., Le N., Lennon G., Marra M., Martin J., Moore B.,
, Schellenberg K., Steptoe M., Tan F., Theising R., White Y., Wylie
, T., Waterston R. and Wilson R.
WashU-Merck EST Project 1997
Unpublished
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through HLNI ; contact the
IMAGE Consortium ([info@image.llnl.gov](#)) for further information.
Seq primer: -26mJ revZ ET from Amersham
High quality sequence stop: 416.
Location/Qualifiers

FEATURES

source

1..443

/organism="Homo sapiens"

/no_type="RNA"

/db_xref="GB:6040267"

/db_xref="taxon:9606"

/clone="IMAGE:796263"

/dev_stage="8-9 weeks"

/lab_host="DH10B"

/clone_1lb="Soares_total_fetus_Nb2HFg_9w"

/note="Vector: pRTD-Poc (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5']
TGTTCAATCATCGAATGCCAGCCGCTTAATTTTTTTTTTTTTT 3').
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I

Alignment Scores:

Pred. No.: 0.00612 Length: 475
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AA452391 (1-475)

Oy 1 ThralAcyllethrrValGluAspAlaGlu 10
 Db 248 ACAGCCTGTATCAGTGAAGATGCAGAA 277

RESULT 14
 AA452391 504 bp mRNA linear EST 05-JUN-1997
 LOCUS 2249C10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
 DEFINITION IMAGE:787890 5', mRNA sequence.

ACCESSION AA452391
 VERSION AA452391.1 GI:2166060
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 504)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maria, M., Martin, J., Moore, B., Schellenberg, R., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
 Washu-Merck EST Project 1997

TITLE JOURNAL
 COMMENT Contact: Wilson R.
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

FEATURES
 source Email: est@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 472.

Location/Qualifiers
 1. 504
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:5985507"
 /db_xref="taxon:9606"
 /clone="IMAGE:787890"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares_total_fetus_Nb2HF8_9w"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from pooled 8-9 week
 (total) fetus material with a Not I - oligo(dT) primer [5'
 TGTTCACATCTGAATGGAGCGCCGCTTAATTTTITTTTITTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 136 a 107 c 141 g 120 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.00651 Length: 504
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x AA452391 (1-504)

Oy 1 ThralAcyllethrrValGluAspAlaGlu 10
 Db 11 ACAGCCTGTATCAGTGAAGATGCAGAA 40

RESULT 15
 BU696863 524 bp mRNA linear EST 09-OCT-2002
 LOCUS LUZ1n13969T7 Hematopoietic Stem Cell Subtracted Library Mus
 DEFINITION musculus cDNA 5' similar to hematopoietic lineage switch 2, mRNA
 sequence.

ACCESSION BU696863
 VERSION BU696863.1 GI:23607807
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 524)
 Phillips, R.L., Ernst, R.E., Brunk, B.P., Ivanova, N., Mahan, M.A., Deanehan, J.K., Moore, K.A., Overton, G.C., and Lemischka, I.R.
 The genetic program of hematopoietic stem cells
 Science 288 (5471), 1635-1640 (2000)
 MEDLINE 20295303
 PUBMED 10834841

COMMENT Contact: Lemischka, Ihor R.
 Department of Molecular Biology
 Princeton University
 Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
 Tel: 609 258 2838
 Fax: 609 258 2759

TITLE JOURNAL
 COMMENT Email: ilemischka@molbio.princeton.edu
 These ESTs are derived from a subtracted cDNA library enriched for
 gene products expressed in day 14-14.5 fetal liver hematopoietic
 stem cells defined as lineage^{neg}/lo, A4.1pos, ckitpos, ly6A/E
 (Sca-1)pos
 Seq primer: M13Reverse or T7.

FEATURES
 source Location/Qualifiers
 1. 524
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57Bl/6J"
 /db_xref="taxon:10090"
 /tissue_type="Hematopoietic"
 /cell_type="Stem Cells; Lineage^{neg}/lo, A4.1pos, ckitpos, ly6A/E (Sca-1)pos"
 /dev_stage="Embryonic day 14-14.5"
 /lab_host="DH10B"
 /clone_lib="Hematopoietic Stem Cell Subtracted Library"
 /note="Organ: Fetal Liver; Vector: Sport 1; Site 1: Sal I;
 Site 2: Not I; Two directionally cloned cDNA libraries
 were made from fetal liver hematopoietic stem cells
 enriched to be lineage^{neg}/lo, A4.1pos, ckitpos, ly6A/E
 (Sca-1)pos called Scapos and from A4.1neg fetal liver
 cells. Subtractive hybridization was performed by
 hybridization of the target, Scapos, single stranded cDNA
 library in pSport1 to biotinylated RNA transcribed from
 the driver, A4.1neg cDNA library in pSport2 with inserts
 cloned in the complementary orientation. For detailed
 protocols and additional information please see our
 website at <http://stemcell.princeton.edu>."

BASE COUNT 146 a 110 c 140 g 125 t 3 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.00678 Length: 524
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x BU696863 (1-524)

QY 1 ThrAlaCysrIleThrValGluAspAlaGlu 10

Db 353 ACAGCCTGTATCAACGTAGAGATGCAGAA 382

Search completed: December 23, 2003, 12:34:58
Job time : 2050 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2003, 12:00:30 ; Search time 74 Seconds
(without alignments)
59.646 Million cell updates/sec

Title: US-09-745-763-36_COPY_231_240
Perfect score: 10
Sequence: 1 FACITVEDAE 10

Scoring table: OLIGO
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1128671

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=olip2n.rml -MIMATCH=0.1 -LOOPLC=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	1134	4	US-09-482-273-95	Sequence 95, Appl
2	100.0	1863	4	US-09-482-273-28	Sequence 28, Appl
3	60.0	536	3	US-08-714-918-57	Sequence 57, Appl
4	60.0	536	3	US-09-265-315-57	Sequence 57, Appl
5	60.0	536	3	US-09-265-315-57	Sequence 57, Appl
6	60.0	536	3	US-09-265-315-57	Sequence 57, Appl
7	60.0	1021	3	US-08-714-918-70	Sequence 70, Appl
8	60.0	1021	3	US-08-714-918-70	Sequence 70, Appl
9	60.0	1021	3	US-09-265-315-70	Sequence 70, Appl
10	60.0	1021	3	US-09-265-315-70	Sequence 70, Appl
11	60.0	1056	4	US-09-252-991A-14680	Sequence 14680, A
12	60.0	1595	4	US-09-461-325-17	Sequence 17, Appl

C 13	60.0	1650	4	US-09-328-352-1770	Sequence 1770, Ap
C 14	60.0	1968	4	US-09-252-991A-15074	Sequence 15074, A
C 15	60.0	2585	2	US-08-579-777A-1	Sequence 1, Appl1
C 16	60.0	3206	1	US-08-373-134D-1	Sequence 1, Appl1
C 17	60.0	3206	2	US-09-114-637-1	Sequence 1, Appl1
C 18	60.0	3900	4	US-09-252-991A-14550	Sequence 14550, A
C 19	60.0	5115	3	US-08-348-518C-3	Sequence 3, Appl1
C 20	60.0	5115	3	US-08-476-509B-3	Sequence 3, Appl1
C 21	60.0	7042	3	US-09-092-508-1	Sequence 1, Appl1
C 22	60.0	7042	4	US-09-435-115-1	Sequence 1, Appl1
C 23	60.0	7042	4	US-09-098-310-1	Sequence 1, Appl1
C 24	60.0	7042	4	US-09-590-364-21	Sequence 21, Appl
C 25	60.0	7075	3	US-09-092-508-15	Sequence 15, Appl
C 26	60.0	7075	4	US-09-435-115-15	Sequence 15, Appl
C 27	50.0	20	2	US-08-651-692-36	Sequence 36, Appl
C 28	50.0	25	3	US-08-879-941-6	Sequence 6, Appl1
C 29	50.0	25	4	US-09-747-116-6	Sequence 6, Appl1
C 30	50.0	47	4	US-09-422-978-1729	Sequence 1729, Ap
C 31	50.0	147	3	US-09-020-956-57	Sequence 57, Appl
C 32	50.0	147	3	US-09-030-607-57	Sequence 57, Appl
C 33	50.0	147	4	US-09-439-313-57	Sequence 57, Appl
C 34	50.0	147	4	US-09-352-616A-57	Sequence 57, Appl
C 35	50.0	147	4	US-09-232-149A-57	Sequence 57, Appl
C 36	50.0	168	4	US-09-736-457-117	Sequence 117, App
C 37	50.0	168	4	US-09-702-705-117	Sequence 117, App
C 38	50.0	171	4	US-09-702-705-1437	Sequence 1437, Ap
C 39	50.0	171	4	US-09-736-457-1437	Sequence 1437, Ap
C 40	50.0	213	2	US-08-727-688-3	Sequence 3, Appl1
C 41	50.0	214	2	US-08-727-688-2	Sequence 2, Appl1
C 42	50.0	258	4	US-09-134-001C-1695	Sequence 1695, Ap
C 43	50.0	264	1	US-08-700-575-24	Sequence 24, Appl
C 44	50.0	269	4	US-09-016-434-78	Sequence 78, Appl
C 45	50.0	271	4	US-09-506-729-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-482-273-95
Sequence 95, Application US/09482273
Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 95
LENGTH: 1134
TYPE: DNA
ORGANISM: Homo sapiens
US-09-482-273-95

Alignment Scores:

Pred. No.: 0.00194
Score: 10.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-482-273-95 (1-1134)

Qy 1 Thr1aCys1e1n1r1v1a1g1u1a1s1p1a1g1u 10
Db 61 ACAGCCTGTATTACGTCGGAAGATGACGAA 90

RESULT 2
US-09-482-273-28
Sequence 28, Application US/09482273
Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1998-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 1863
TYPE: DNA
ORGANISM: Homo sapiens
US-09-482-273-28

Alignment Scores:
Pred. No.: 0.00297 Length: 1863
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-482-273-28 (1-1863)

Qy 1 Thr1aCys1e1n1r1v1a1g1u1a1s1p1a1g1u 10
Db 789 ACAGCCTGTATTACGTCGGAAGATGACGAA 818

RESULT 3
US-08-714-918-57/c
Sequence 57, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vang
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-57

Alignment Scores:
Pred. No.: 41.6 Length: 536
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 3 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-08-714-918-57 (1-536)

Qy 5 Thr1a1g1u1a1s1p1a1g1u 10
Db 254 ACTGTAGAAGATGCTGAA 237

RESULT 4
US-09-265-315-57/c
Sequence 57, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vang J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-57

Alignment Scores:
Pred. No.: 41.6 Length: 536
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 3 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-265-315-57 (1-536)

QY 5 ThValGluSpAlaGlu 10
Db 254 ACTGTAGAGATGCTGAA 237

RESULT 5
US-09-265-315-57/c
Sequence 57, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmidt, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-57

Alignment Scores:
Pred. No.: 41.6 Length: 536
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 3 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-265-315-57 (1-536)

QY 5 ThValGluSpAlaGlu 10
Db 254 ACTGTAGAGATGCTGAA 237

RESULT 6
US-09-266-417-57/c
Sequence 57, Application US/09266417
Patent No. 6228588
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmidt, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-57

Alignment Scores:
Pred. No.: 41.6 Length: 536
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 3 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-266-417-57 (1-536)

Oy 5 ThvAlGluAepAlaGlu 10
Db 254 ACTGTAGAGATGCTGAA 237

RESULT 7
US-08-714-918-70/c
Sequence 70, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vang
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 1021 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-70

Alignment Scores:
Pred. No.: 72.5 Length: 1021
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 3 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-08-714-918-70 (1-1021)

Oy 5 ThvAlGluAepAlaGlu 10
Db 93 ACTGTAGAGATGCTGAA 76

RESULT 8
US-09-265-315-70/c
Sequence 70, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vang J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:

LENGTH: 1021 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-70

Alignment Scores:
Pred. No.: 72.5 Length: 1021
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 3 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-265-315-70 (1-1021)

QY 5 ThYvAlGluAspAlaGlu 10
|||||
DB 93 ACTGTAGAGATGCTGAA 76

RESULT 9
US-09-265-315-70/c
Sequence 70, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vang J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 1021 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-09-265-315-70

Alignment Scores:
Pred. No.: 72.5 Length: 1021
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 3 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-265-315-70 (1-1021)

QY 5 ThYvAlGluAspAlaGlu 10
|||||
DB 93 ACTGTAGAGATGCTGAA 76

RESULT 10
US-09-266-417-70/c
Sequence 70, Application US/09266417
Patent No. 6228588
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vang J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 1021 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-70

Alignment Scores:

Pred. No.: 72.5 Length: 1021
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 3 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-266-417-70 (1-1021)

QY 5 ThrValGIuAspAlaGlu 10
Db 93 ACTGTAGAGATGCTGAA 76

RESULT 11

US-09-252-991A-14680
Sequence 14680, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 14680
LENGTH: 1056
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14680

Alignment Scores:

Pred. No.: 74.6 Length: 1056
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 4 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-252-991A-14680 (1-1056)

QY 4 lIeThrValGIuAspAla 9
Db 265 ATCACGTCGAGATGCC 282

RESULT 12

US-09-461-325-17/C
Sequence 17, Application US/09461325A
Patent No. 6475753
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P202991
CURRENT APPLICATION NUMBER: US/09/461.325A
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113

EARLIER FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 1595
TYPE: DNA
ORGANISM: Homo sapiens
US-09-461-325-17

Alignment Scores:

Pred. No.: 106 Length: 1595
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 4 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-461-325-17 (1-1595)

QY 1 ThrAlaCysIleThrVal 6
Db 827 ACACATGATCACTGTC 810

RESULT 13

US-09-328-352-1770/C
Sequence 1770, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328.352
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1770
LENGTH: 1650
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-1770

Alignment Scores:

Pred. No.: 110 Length: 1650
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 4 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-328-352-1770 (1-1650)

QY 2 AlaCysIleThrValGlu 7
Db 348 GCTTGATCAGCGTCGAG 331

RESULT 14

US-09-252-991A-15074/C
Sequence 15074, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15074
LENGTH: 1968

TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15074

Alignment Scores:

Pred. No.:	127	Length:	1968
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.00%	Indels:	0
DB:	4	Gaps:	0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-252-991A-15074 (1-1968)

QY 4 |||||
DB 1506 ATCACCCTCGAGATGCC 1489

RESULT 15

US-08-579-777A-1
Sequence 1, Application US/08579777A

Patent No. 5912153

GENERAL INFORMATION:

APPLICANT: Enderlin, Carol S.

TITLE OF INVENTION: (1.3)B-glucan synthase genes and

TITLE OF INVENTION: inducible inhibition of fungal growth using the antisense

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Davis, Graham & Stubbs L.L.P.

STREET: 370 Seventeenth Street

CITY: Denver

STATE: Colorado

COUNTRY: U.S.A.

ZIP: 80201-0185

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/579,777A

FILING DATE: 28-DEC-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/155,004

FILING DATE: 18-NOV-1993

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303)892-7370

TELEFAX: (303)893-1379

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2585 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Neurospora crassa

STRAIN: wild-type 74-DR 23-1VA

DEVELOPMENTAL STAGE: Mycelial

IMMEDIATE SOURCE:

LIBRARY: lambda Zap CDNA

CLONE: gs-1

POSITION IN GENOME:

CHROMOSOME/SEGMENT: linkage group V

US-08-579-777A-1

Alignment Scores:

Pred. No.: 161

Length: 2585

Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.00%	Indels:	0
DB:	2	Gaps:	0

US-09-745-763-36_COPY_231_240 (1-10) x US-08-579-777A-1 (1-2585)

QY 5 ThVaIGluAspAlaGlu 10
DB 1697 ACAGTCGAAGACCGCGAG 1714

Search completed: December 23, 2003, 12:40:52
Job time : 76 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2003, 12:00:30 ; Search time 2486 Seconds
(without alignments)
13.404 Million cell updates/sec

Title: US-09-745-763-36_COPY_231_240
Perfect score: 10
Sequence: 1 TACTIVEDAB 10

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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2211978 segs, 1666101734 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4410318

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
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-MAXLEN=200000000 -USER=US09745763@cgn1_1_107@runat_23122003_120025_20145
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Database :

Published Applications_NA:*

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- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
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- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
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- 13: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/2/pubpna/US10_NEW_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	10	100.0	1134	11	US-09-984-271-95	Sequence 95, Appl
2	10	100.0	1851	9	US-09-745-763-35	Sequence 35, Appl
3	10	100.0	1863	11	US-09-984-271-28	Sequence 28, Appl
4	6	60.0	37	14	US-10-004-717-69	Sequence 69, Appl
5	6	60.0	61	13	US-10-231-452-23	Sequence 23, Appl
6	6	60.0	98	13	US-10-231-452-47	Sequence 47, Appl
7	6	60.0	297	10	US-09-974-300-3664	Sequence 3664, Ap
8	6	60.0	357	13	US-10-231-452-50	Sequence 50, Appl
9	6	60.0	357	13	US-10-231-452-52	Sequence 52, Appl
10	6	60.0	357	13	US-10-231-452-59	Sequence 59, Appl
11	6	60.0	357	13	US-10-231-452-60	Sequence 60, Appl
12	6	60.0	391	11	US-09-803-719-73	Sequence 73, Appl
13	6	60.0	456	9	US-09-864-761-1999	Sequence 1999, Ap
14	6	60.0	472	11	US-09-918-995-20434	Sequence 20434, A
15	6	60.0	524	10	US-09-867-701-4823	Sequence 4823, Ap
16	6	60.0	609	14	US-10-004-717-14	Sequence 14, Appl
17	6	60.0	612	13	US-10-296-540-4	Sequence 4, Appl
18	6	60.0	653	13	US-10-027-632-228744	Sequence 228744,
19	6	60.0	653	14	US-10-027-632-228744	Sequence 228744,
20	6	60.0	665	13	US-10-027-632-128774	Sequence 128774,
21	6	60.0	665	14	US-10-027-632-128774	Sequence 128774,
22	6	60.0	1194	10	US-09-974-300-1072	Sequence 1072, Ap
23	6	60.0	1299	9	US-09-815-242-7603	Sequence 7603, Ap
24	6	60.0	1489	15	US-10-137-036-125	Sequence 125, App
25	6	60.0	1574	13	US-10-027-632-86669	Sequence 86669, A
26	6	60.0	1574	14	US-10-027-632-86669	Sequence 86669, A
27	6	60.0	1595	15	US-10-012-542-17	Sequence 17, Appl
28	6	60.0	1830	9	US-09-815-242-4504	Sequence 4504, Ap
29	6	60.0	1857	9	US-09-815-242-8469	Sequence 8469, Ap
30	6	60.0	1857	9	US-09-815-242-8469	Sequence 8469, Ap
31	6	60.0	2344	13	US-09-814-353-19093	Sequence 19093, A
32	6	60.0	2477	10	US-09-822-830A-252	Sequence 252, App
33	6	60.0	3302	13	US-09-946-290-131	Sequence 13, Appl
34	6	60.0	3308	10	US-09-771-161A-71	Sequence 71, Appl
35	6	60.0	4116	13	US-10-296-540-3	Sequence 3, Appl
36	6	60.0	4325	13	US-10-296-540-1	Sequence 1, Appl
37	6	60.0	4510	14	US-10-005-983-1	Sequence 1, Appl
38	6	60.0	4638	13	US-10-006-285-403	Sequence 403, App
39	6	60.0	4893	13	US-10-240-965-85	Sequence 85, Appl
40	6	60.0	5049	15	US-10-084-817-174	Sequence 174, App
41	6	60.0	5128	13	US-10-133-937-57	Sequence 57, Appl
42	6	60.0	5128	13	US-10-341-434-156	Sequence 156, App
43	6	60.0	6336	8	US-08-781-986A-219	Sequence 219, App
44	6	60.0	7042	10	US-09-876-667-1	Sequence 1, Appl
45	6	60.0	7042	12	US-10-441-281-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-984-271-95
; Sequence 95, Application US/09984271
; Publication No. US20030040088A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: PZ030P1
; CURRENT APPLICATION NUMBER: US/09/984, 271
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/482, 273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092, 921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092, 922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092, 956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 1134

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TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-271-95

Alignment Scores:
Pred. No.: 0.00641 Length: 1134
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-984-271-95 (1-1134)

QY 1 ThrAlaCysIleThrValGluAspAlaGlu 10
Db 61 ACAGCCTGTATTACGGTGGAAGATGCAGAA 90

RESULT 2
US-09-745-763-35
Sequence 35, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
McCoy, John M.
Lavallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
City: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Alignment Scores:
Pred. No.: 0.00984 Length: 1851
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9
TYPE: DNA

```

```

US-09-745-763-36_COPY_231_240 (1-10) x US-09-745-763-35 (1-1851)

QY 1 ThrAlaCysIleThrValGluAspAlaGlu 10
Db 789 ACAGCCTGTATTACGGTGGAAGATGCAGAA 818

RESULT 3
US-09-984-271-28
Sequence 28, Application US/09984271
Publication No. US20030040088A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 1863
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-271-28

Alignment Scores:
Pred. No.: 0.0099 Length: 1863
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 11
TYPE: DNA

US-09-745-763-36_COPY_231_240 (1-10) x US-09-984-271-28 (1-1863)

QY 1 ThrAlaCysIleThrValGluAspAlaGlu 10
Db 789 ACAGCCTGTATTACGGTGGAAGATGCAGAA 818

RESULT 4
US-10-004-717-69/c
Sequence 69, Application US/10004717
Publication No. US20020192665A1
GENERAL INFORMATION:
APPLICANT: ZOCHBI, HUDA Y.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN
ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: P01899U54
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 37
TYPE: DNA

```

ORGANISM: Homo sapiens
US-10-004-717-69
Alignment Scores:
Pred. No.: 13.5
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 60.00%
DB: 14
Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-10-004-717-69 (1-37)

Qy 1 Thra1Cys1eThra1 6
Db 27 ACCGATGCTACTGTC 10

RESULT 5
US-10-231-452-23
Sequence 23, Application US/10231452
Publication No. US20030175273A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: HOSAKA, EMI
APPLICANT: TANAKA, AKIKO
APPLICANT: KOIKE, MASAMICHI
TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF
FILE REFERENCE: 249-273
CURRENT APPLICATION NUMBER: US/10/231,452
CURRENT FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: JP 2001-265144
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 61
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
US-10-231-452-23

Alignment Scores:
Pred. No.: 20.9
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 60.00%
DB: 13
Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-10-231-452-23 (1-61)

Qy 3 Cys1eThra1Gluasp 8
Db 44 TGTATTACTGTGAGAGAC 61

RESULT 6
US-10-231-452-47
Sequence 47, Application US/10231452
Publication No. US20030175273A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: HOSAKA, EMI
APPLICANT: TANAKA, AKIKO
APPLICANT: KOIKE, MASAMICHI
TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF
FILE REFERENCE: 249-273
CURRENT APPLICATION NUMBER: US/10/231,452
CURRENT FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: JP 2001-265144
PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 98
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
US-10-231-452-47

Alignment Scores:
Pred. No.: 31.7
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 60.00%
DB: 13
Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-10-231-452-47 (1-98)

Qy 3 Cys1eThra1Gluasp 8
Db 61 TGTATTACTGTGAGAGAC 78

RESULT 7
US-09-974-300-3664
Sequence 3664, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085-500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3664
LENGTH: 297
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-3664

Alignment Scores:
Pred. No.: 83.7
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 60.00%
DB: 10
Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-974-300-3664 (1-297)

Qy 5 Thra1Gluasp1aglu 10
Db 74 ACTGTGAGAGAGCGCTGAG 91

RESULT 8
US-10-231-452-50
Sequence 50, Application US/10231452
Publication No. US20030175273A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: HOSAKA, EMI
APPLICANT: TANAKA, AKIKO
APPLICANT: KOIKE, MASAMICHI
TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF

FILE REFERENCE: 249-273
CURRENT APPLICATION NUMBER: US/10/231,452
CURRENT FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: JP 2001-265144
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 357
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
NAME/KEY: CDS
LOCATION: (1)..(357)
US-10-231-452-50

Alignment Scores:
Pred. No.: 98.4 Length: 357
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 13 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-10-231-452-50 (1-357)

QY 3 Cys11eThrValGluAsp 8
|||
278 TGTATTACTGTGGAAGAC 295

RESULT 9
US-10-231-452-52
Sequence 52, Application US/10231452
Publication No. US20030175273A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: HOSAKA, EMI
APPLICANT: TANAKA, AKIKO
APPLICANT: KOIKE, MASAMICHI
TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF
FILE REFERENCE: 249-273
CURRENT APPLICATION NUMBER: US/10/231,452
CURRENT FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: JP 2001-265144
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52
LENGTH: 357
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
NAME/KEY: CDS
LOCATION: (1)..(357)
US-10-231-452-52

Alignment Scores:
Pred. No.: 98.4 Length: 357
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 13 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-10-231-452-52 (1-357)

QY 3 Cys11eThrValGluAsp 8
|||
278 TGTATTACTGTGGAAGAC 295

Db 278 TGTATTACTGTGGAAGAC 295

RESULT 10
US-10-231-452-59
Sequence 59, Application US/10231452
Publication No. US20030175273A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: HOSAKA, EMI
APPLICANT: TANAKA, AKIKO
APPLICANT: KOIKE, MASAMICHI
TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF
FILE REFERENCE: 249-273
CURRENT APPLICATION NUMBER: US/10/231,452
CURRENT FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: JP 2001-265144
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 357
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
NAME/KEY: CDS
LOCATION: (1)..(357)
US-10-231-452-59

Alignment Scores:
Pred. No.: 98.4 Length: 357
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 13 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-10-231-452-59 (1-357)

QY 3 Cys11eThrValGluAsp 8
|||
278 TGTATTACTGTGGAAGAC 295

RESULT 11
US-10-231-452-60
Sequence 60, Application US/10231452
Publication No. US20030175273A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: HOSAKA, EMI
APPLICANT: TANAKA, AKIKO
APPLICANT: KOIKE, MASAMICHI
TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF
FILE REFERENCE: 249-273
CURRENT APPLICATION NUMBER: US/10/231,452
CURRENT FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: JP 2001-265144
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 60
LENGTH: 357
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
NAME/KEY: CDS
LOCATION: (1)..(357)
US-10-231-452-60

Alignment Scores:

Pred. No.: 98.4 Length: 357
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.00% Indels: 0
 DB: 13 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-10-231-452-60 (1-357)

QY 3 Cys11eThralValGuap 8

Db 278 TGTATCTACTGTGGAAGAC 295

RESULT 12

US-09-803-719-73/c

; Sequence 73, Application US/09803719
 ; Publication No. US20030044783A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Lewis T.
 ; APPLICANT: Escobedo, Jaime
 ; APPLICANT: Innis, Michael A.
 ; APPLICANT: Garcia, Pablo Dominguez
 ; APPLICANT: Sudduth-Klinger, Julie
 ; APPLICANT: Reinhard, Christoph
 ; APPLICANT: Giese, Klaus
 ; APPLICANT: Randazzo, Filippo
 ; APPLICANT: Kennedy, Giulia C.
 ; APPLICANT: Pct, David
 ; APPLICANT: Kaasam, Alcat
 ; APPLICANT: Lamson, George
 ; APPLICANT: Drmanac, Radoje
 ; APPLICANT: Ckvenjakov, Radomir
 ; APPLICANT: Dickson, Mark
 ; APPLICANT: Drmanac, Snezana
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Leshkowitz, Dena
 ; APPLICANT: Kita, David
 ; APPLICANT: Garcia, Veronica
 ; APPLICANT: Jones, Lee William
 ; APPLICANT: Stache-Crain, Birgit
 ; TITLE OF INVENTION: Human Genes and Gene Products
 ; FILE REFERENCE: 1624, 002
 ; CURRENT APPLICATION NUMBER: US/09/803,719
 ; PRIOR FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: 60/188,609
 ; NUMBER OF SEQ ID NOS: 2396
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 73
 ; LENGTH: 391
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-803-719-73

Alignment Scores:

Pred. No.: 107 Length: 391
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.00% Indels: 0
 DB: 11 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-803-719-73 (1-391)

QY 1 ThralaCys11eThral 6

Db 218 ACAGCTTGACATCACTGTC 201

RESULT 13

US-09-864-761-1999

; Sequence 1999, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aecmca-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263,6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 1999
 ; LENGTH: 456
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AP000403.1
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
 ; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
 ; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

US-09-864-761-1999

Alignment Scores:

Pred. No.: 122 Length: 456
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.00% Indels: 0
 DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-864-761-1999 (1-456)

Oy 1 ThrValGluAspAlaGlu 6

Db 176 ACAGCTCGAGATGCTGAG 193

RESULT 14

US-09-918-995-20434/C
 ; Sequence 20434, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918, 995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235, 076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 20434
 ; LENGTH: 472
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(472)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-20434

Alignment Scores:

Pred. No.: 126 Length: 472
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.00% Indels: 0
 DB: 11 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-918-995-20434 (1-472)

Oy 5 ThrValGluAspAlaGlu 10

Db 302 ACTGTCGAGATGCTGAG 285

RESULT 15

US-09-867-701-4823/C
 ; Sequence 4823, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agiate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867, 701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4823
 ; LENGTH: 524
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-867-701-4823

Alignment Scores:

Pred. No.: 138 Length: 524
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.00% Indels: 0

DB: 10 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x US-09-867-701-4823 (1-524)

Oy 5 ThrValGluAspAlaGlu 10

Db 144 ACTGTCGAGATGCTGAG 127

Search completed: December 23, 2003, 13:47:21
 Job time: 2487 secs